

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 29, 2006, 14:01:34 ; Search time 49 Seconds  
(without alignments)  
464.448 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKNGYGTWSK.....TNSQVRWEYCKIPSCDSPPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles.pep:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1540	100.0	260	2	US-09-982-516-1
2	1535	99.7	339	1	US-08-248-628A-3
3	1535	99.7	339	1	US-08-451-932-3
4	1535	99.7	339	1	US-08-452-260-3
5	1535	99.7	339	1	US-08-326-785-3
6	1535	99.7	339	1	US-08-612-788-3
7	1535	99.7	339	1	US-08-605-598B-3
8	1535	99.7	339	1	US-08-429-743-3
9	1535	99.7	339	1	US-08-866-735-3
10	1535	99.7	339	2	US-09-066-028-3
11	1535	99.7	339	2	US-09-335-325-3
12	1535	99.7	339	2	US-09-335-614-3
13	1535	99.7	339	5	PCT-US95-05107-3
14	1535	99.7	374	2	US-09-377-250-3
15	1535	99.7	375	2	US-09-377-250-2
16	1535	99.7	378	1	US-08-612-788-42
17	1535	99.7	378	2	US-09-066-028-42
18	1535	99.7	378	2	US-09-206-059-1
19	1535	99.7	378	2	US-09-335-325-42
20	1535	99.7	378	2	US-09-335-614-42
21	1535	99.7	451	2	US-09-377-250-1
22	1535	99.7	452	2	US-09-377-250-4
23	1535	99.7	568	3	US-09-946-893C-5
24	1535	99.7	570	3	US-09-946-893C-8
25	1535	99.7	575	3	US-09-946-893C-6
26	1535	99.7	790	1	US-08-469-486-54

27	1535	99.7	790	1	US-08-469-658-54	Sequence 54, Appli
28	1535	99.7	791	1	US-08-643-219-1	Sequence 1, Appli
29	1535	99.7	791	1	US-09-131-995-1	Sequence 1, Appli
30	1535	99.7	791	1	US-08-832-087B-1	Sequence 1, Appli
31	1535	99.7	791	2	US-08-851-350-1	Sequence 1, Appli
32	1535	99.7	791	2	US-09-132-154-1	Sequence 1, Appli
33	1535	99.7	791	2	US-08-991-761A-6	Sequence 6, Appli
34	1535	99.7	791	2	US-08-924-287A-1	Sequence 1, Appli
35	1535	99.7	791	2	US-10-360-101-257	Sequence 257, App
36	1535	99.7	810	1	US-07-854-603-2	Sequence 2, Appli
37	1535	99.7	810	1	US-08-147-000B-29	Sequence 29, Appli
38	1535	99.7	810	2	US-09-086-514-1	Sequence 1, Appli
39	1535	99.7	810	2	US-09-192-013-5	Sequence 5, Appli
40	1535	99.7	810	2	US-09-403-736-1	Sequence 1, Appli
41	1535	99.7	810	2	US-09-701-265-1	Sequence 1, Appli
42	1535	99.7	810	3	US-09-946-893C-2	Sequence 2, Appli
43	1535	99.7	814	1	US-08-750-711-1	Sequence 1, Appli
44	1532	99.5	713	2	US-09-949-016-9983	Sequence 9983, Ap
45	1531	99.4	369	2	US-09-701-265-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-982-516-1  
; Sequence 1, Application US/09982516  
; Patent No. 6723536

GENERAL INFORMATION:  
; APPLICANT: Madsen, John  
; APPLICANT: Liang, Hong  
; APPLICANT: Sim, Kim Lee

; APPLICANT: Zhou, Xinhua  
; APPLICANT: Chang-Murad, Amy  
; APPLICANT: Boerner, Renee J.

; APPLICANT: Bernero, Lourdes L.  
; APPLICANT: Mistry, Firoz R.  
; APPLICANT: Schrimsher, Jeffrey L.

; APPLICANT: Shepard, Scott R.

; TITLE OF INVENTION: Method of Producing and Purifying Angiotensin Protein  
; FILE REFERENCE: 05213-0562 43170-264313  
; CURRENT APPLICATION NUMBER: US/09/982,516

; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: PCT/US00/32843

; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: US 60/168,919

; PRIOR FILING DATE: 1999-12-03  
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1

; LENGTH: 260  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-982-516-1

Query Match 100.0%; Score 1540; DB 2; Length 260;  
Best Local Similarity 100.0%; Pred. No. 3.6e-139;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VYLSECKTGNGKNGYGTWSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
Db	1	VYLSECKTGNGKNGYGTWSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
Qy	61	DPQGPWCYTTDEKRYDYCDILEECBECMHCSENGYDGIKSTMSGLEQAWDSQSPHAAH	120
Db	61	DPQGPWCYTTDEKRYDYCDILEECBECMHCSENGYDGIKSTMSGLEQAWDSQSPHAAH	120
Qy	121	GYIPSKFPNKLKQNYCRNPDELRCPCCTTDPNKKWELCDIPRCTTPPPSGGTYQCLK	180
Db	121	GYIPSKFPNKLKQNYCRNPDELRCPCCTTDPNKKWELCDIPRCTTPPPSGGTYQCLK	180
Qy	181	GTGENTRGVATVSGHTCOHWSAQTPHHTERTPFPCCKNLIDENYCRPDGGRAPWCHT	240

Db 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPFPCKNLNDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 2

US-08-248-629A-3  
; Sequence 3, Application US/08248629A  
; Patent No. 5639725  
; GENERAL INFORMATION:  
; APPLICANT: Folkman, Judah  
; APPLICANT: O'Reilly, Michael  
; TITLE OF INVENTION: Angiostatin and Method of Use  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1769  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50  
; COMPUTER: MacIntosh  
; OPERATING SYSTEM: 7.0  
; SOFTWARE: Microsoft Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/248,629A  
; FILING DATE: 04/26/94  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Larry W. Stults, Ph.D.  
; REGISTRATION NUMBER: 34,025  
; REFERENCE/DOCKET NUMBER: 05213-0120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-248-629A-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENYDGIKSKTMSGLECQAWDSQSPH 120  
Db 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENYDGIKSKTMSGLECQAWDSQSPH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPSSGPTYOCLK 180  
Db 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPSSGPTYOCLK 180  
QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPFPCKNLNDENYCRNPDGKRAPWCHT 240

RESULT 4

US-08-452-260-3  
; Sequence 3, Application US/08452260  
; Patent No. 5776704

RESULT 3

US-08-451-932-3  
; Sequence 3, Application US/08451932  
; Patent No. 5733876  
; GENERAL INFORMATION:  
; APPLICANT: Folkman, Judah  
; APPLICANT: O'Reilly, Michael  
; TITLE OF INVENTION: Method of Treating an Angiogenic  
; TITLE OF INVENTION: Disease  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1769  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50  
; COMPUTER: MacIntosh  
; OPERATING SYSTEM: 7.0  
; SOFTWARE: Microsoft Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/451,932  
; FILING DATE: 05/26/95  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/248,629  
; FILING DATE: 04/26/94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Larry W. Stults, Ph.D.  
; REGISTRATION NUMBER: 34,025  
; REFERENCE/DOCKET NUMBER: 05213-0123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-451-932-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENYDGIKSKTMSGLECQAWDSQSPH 120  
Db 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENYDGIKSKTMSGLECQAWDSQSPH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPSSGPTYOCLK 180  
Db 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPSSGPTYOCLK 180  
QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 4

US-08-452-260-3  
; Sequence 3, Application US/08452260  
; Patent No. 5776704

GENERAL INFORMATION:  
APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Method of Diagnosing an Angiogenic  
Disease  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,260  
FILING DATE: 05/26/95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,629  
FILING DATE: 04/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Stults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-452-260-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGGPMCYTTDPKRYDYCDILLECEBECMHCSGENYDGKISKTMSGLECOAWDSQSPH 120  
Db 61 DPGGPMCYTTDPKRYDYCDILLECEBECMHCSGENYDGKISKTMSGLECOAWDSQSPH 120  
QY 121 GYIPSKFPNKLKQNYCRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GYIPSKFPNKLKQNYCRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5  
US-08-326-785-3  
Sequence 3, Application US/08326785  
Patent No. 5792845  
GENERAL INFORMATION:  
APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/326,785  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,629  
FILING DATE: 04/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Stults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-326-785-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGGPMCYTTDPKRYDYCDILLECEBECMHCSGENYDGKISKTMSGLECOAWDSQSPH 120  
Db 61 DPGGPMCYTTDPKRYDYCDILLECEBECMHCSGENYDGKISKTMSGLECOAWDSQSPH 120  
QY 121 GYIPSKFPNKLKQNYCRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GYIPSKFPNKLKQNYCRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6  
US-08-612-788-3  
Sequence 3, Application US/08612788  
Patent No. 5837682  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: O'Reilly, Micheal  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta

STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment

US-08-612-788-3  
Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPON 60  
Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPON 60  
QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120  
Db 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120  
QY 121 GIYPSKFPNKLKNGYCRNPDRRLRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GIYPSKFPNKLKNGYCRNPDRRLRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDKGRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDKGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7  
US-08-605-598B-3  
Sequence 3, Application US/08605598B  
Patent No. 5861372  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: Lin, Jie  
APPLICANT: O'Reilly, Michael S.  
TITLE OF INVENTION: Aggregate Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.

CITY: Atlanta  
COUNTRY: Georgia  
STATE: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,598B  
FILING DATE: 22-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0127  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human Angiostatin

US-08-605-598B-3  
Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPON 60  
Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPON 60  
QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120  
Db 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120  
QY 121 GIYPSKFPNKLKNGYCRNPDRRLRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GIYPSKFPNKLKNGYCRNPDRRLRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDKGRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDKGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8  
US-08-429-743-3  
Sequence 3, Application US/08429743  
Patent No. 5885795  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael  
APPLICANT: Folkman, M. Judah  
APPLICANT: Sim, Kim Lee  
APPLICANT: Cao, Yihai  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.

STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/429,743  
FILING DATE: 20-OCT-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,629  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/326,785  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Johnson, James D.  
REGISTRATION NUMBER: 31,771  
REFERENCE/DOCKET NUMBER: 05213-0122  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CLONE: Angiotatin fragment  
US-08-429-743-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60

QY 61 DQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLEQAWDSQSPH 120  
DB 61 DQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLEQAWDSQSPH 120

QY 121 GYIPSKFPNNLKNKNCYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180  
DB 121 GYIPSKFPNNLKNKNCYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9  
US-08-866-735-3  
Sequence 3, Application US/08866735  
Patent No. 5945403  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Angiotatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta

STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/866,735  
FILING DATE: 30-MAY-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05940-0129  
TELEPHONE: (404) 818-3700  
TELEFAX: (404) 818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiotatin fragment  
US-08-866-735-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60

QY 61 DQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLEQAWDSQSPH 120  
DB 61 DQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLEQAWDSQSPH 120

QY 121 GYIPSKFPNNLKNKNCYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180  
DB 121 GYIPSKFPNNLKNKNCYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 10  
US-09-066-028-3  
Sequence 3, Application US/09066028  
Patent No. 6024688  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: O'Reilly, Michael  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, B. Kim Lee  
TITLE OF INVENTION: Angiotatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
US-09-066-028-3

Query Match 99.7%; Score 1535; DB 2; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILLECEECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 120  
DB 61 DPQGPWCYTTDPKRYDYCDILLECEECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCCLK 180  
DB 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 11  
US-09-335-325-3  
Sequence 3, Application US/09335325  
Patent No. 6521439  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
O'Reilly, Micheal  
Cao, Yihai

Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,325  
FILING DATE: 17-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 2; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILLECEECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 120  
DB 61 DPQGPWCYTTDPKRYDYCDILLECEECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCCLK 180  
DB 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 12  
US-09-335-614-3

Sequence 3, Application US/09335614  
Patent No. 6949511  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
O'Reilly, Micheal  
Cao, Yihai  
Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,614  
FILING DATE: 18-Jun-1999  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-335-614-3

Query Match 99.7%; Score 1535; DB 2; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECOAWDSQSPHAH 120  
DB 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECOAWDSQSPHAH 120  
QY 121 GYIPKFPNNKLNKYNCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
DB 121 GYIPKFPNNKLNKYNCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260  
RESULT 13  
PCT-US95-05107-3  
Sequence 3, Application PC/TUS9505107  
GENERAL INFORMATION:  
APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05107  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,629  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/326,785  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Johnson, James D.  
REGISTRATION NUMBER: 31,771  
REFERENCE/DOCKET NUMBER: 05213-0122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PCT-US95-05107-3

Query Match 99.7%; Score 1535; DB 5; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.5e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECOAWDSQSPHAH 120  
DB 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECOAWDSQSPHAH 120  
QY 121 GYIPKFPNNKLNKYNCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
DB 121 GYIPKFPNNKLNKYNCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260  
|||||

RESULT 14  
US-09-377-250-3  
; Sequence 3, Application US/09377250  
; Patent No. 6365364  
; GENERAL INFORMATION:  
; APPLICANT: MANN, KENNETH G.  
; APPLICANT: SWORDS JENNY, NANCY  
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF  
; FILE REFERENCE: 48409/360  
; CURRENT APPLICATION NUMBER: US/09/377,250  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: angiogenesis inhibitor  
; NAME/KEY: MOD RES  
; LOCATION: (264)  
; OTHER INFORMATION: Xaa = Gln or Glu  
US-09-377-250-3

Query Match 99.7%; Score 1535; DB 2; Length 374;  
Best Local Similarity 99.6%; Pred. No. 1.7e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPH 120  
Db 61 DPGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180  
Db 121 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 15  
US-09-377-250-2  
; Sequence 2, Application US/09377250  
; Patent No. 6365364  
; GENERAL INFORMATION:  
; APPLICANT: MANN, KENNETH G.  
; APPLICANT: SWORDS JENNY, NANCY  
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF  
; FILE REFERENCE: 48409/360  
; CURRENT APPLICATION NUMBER: US/09/377,250  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: angiogenesis inhibitor

; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (265)  
; OTHER INFORMATION: Xaa = Gln or Glu  
US-09-377-250-2  
Query Match 99.7%; Score 1535; DB 2; Length 375;  
Best Local Similarity 99.6%; Pred. No. 1.7e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
Db 2 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 61  
QY 61 DPGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPH 120  
Db 62 DPGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPH 121  
QY 121 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180  
Db 122 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 181  
QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 182 GTGENYRGNAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLNDENYCRNPDGKRAPWCHT 241  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 242 TNSQVRWEYCKIPSCDSSPV 261

Search completed: August 29, 2006, 14:02:54  
JOB time : 50 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2006, 13:53:08 ; Search time 299 Seconds

(without alignments)  
804.361 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VTLSEKGTGNGNVRGTWSK.....TNSQVRWEYCKIPSCDSFV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	1535	99.7	810	1	PLMN HUMAN
2	1535	99.7	810	2	Q5TEH4 HUMAN
3	1458	94.7	810	2	Q5R8X6 PONGO PYGMA
4	1442	93.6	810	1	PLMN MACMU
5	1306	84.8	359	2	Q8WNR1 CANIS FAMIL
6	1299	84.4	812	1	PLMN RAT
7	1299	84.4	812	2	Q5BK86 RAT
8	1292	83.9	790	1	PLMN FIG
9	1291	83.8	812	1	PLMN BOVIN
10	1279	83.1	466	2	Q6TC10 MOUSE
11	1279	83.1	812	1	PLMN MOUSE
12	1279	83.1	812	2	Q3VLT9 MOUSE
13	1237	80.3	810	1	PLMN ERIEU
14	1203.5	78.1	759	2	Q7TP84 RAT
15	1160	75.3	806	1	PLMN MACREU
16	996	64.7	818	2	Q6PBA6 BRARE
17	962	62.5	797	2	Q5OLG6 ORVLA
18	959	62.3	814	2	Q5DVP8 ONCMY
19	881	57.2	2869	2	Q28398 ERIEU
20	809.5	52.6	449	2	Q6GP14 XENLA
21	809.5	52.6	716	2	Q91691 XENLA
22	797	51.8	728	1	HGF HUMAN
23	796	51.7	709	2	Q72TN9 XENLA
24	795.5	51.7	717	2	P70006 XENLA
25	782	50.8	728	1	HGF RAT
26	778	50.5	726	2	Q90978 CHICK
27	778	50.5	730	2	Q867B7 CANFA
28	777	50.5	728	2	Q8C9G5 MOUSE
29	776.5	50.4	710	2	Q91402 9PIPI
30	776	50.4	728	1	HGF MOUSE
31	776	50.4	728	2	Q53WS5 MOUSE

32	774	50.3	730	2	Q76BS1 BOVIN
33	772	50.1	704	2	Q90865 CHICK
34	772	50.1	728	2	Q9BH09 FELCA
35	766.5	49.8	699	2	Q5RGG3 BRARE
36	766.5	49.8	709	2	Q5XFY1 BRARE
37	766.5	49.8	709	2	Q90ZN6 BRARE
38	766.5	49.8	716	2	P70521 RAT
39	758	49.2	655	2	Q4RX92 TETNG
40	756.5	49.1	716	2	Q3UZ05 MOUSE
41	754.5	49.0	405	2	Q788Q2 CHICK
42	753.5	48.9	716	1	HGFL MOUSE
43	753.5	48.9	716	2	Q6GTL1 MOUSE
44	753.5	48.9	716	2	Q91XG8 MOUSE
45	752	48.8	667	2	Q4SUG4 TETNG

## ALIGNMENTS

### RESULT 1

ID	PLMN HUMAN	STANDARD;	PRT;	810 AA.
AC	P00747; Q15146; Q6PA00;			
DT	21-JUL-1986, integrated into UniProtKB/Swiss-Prot.			
DT	01-JUL-1989, sequence version 2.			
DT	07-MAR-2006, entry version 92.			
DE	Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;			
DE	Activation peptide; Angiostatin; Plasmin heavy chain A, short form;			
DE	Plasmin light chain B].			
GN	Name=PLG;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, AND VARIANT ASN-472.			
RX	MEDLINE=90202879; PubMed=2318848;			
RA	Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;			
RT	"Characterization of the gene for human plasminogen, a key proenzyme			
RT	in the fibrinolytic system.";			
RL	J. Biol. Chem. 265:6104-6111(1990).			
[2]				
RN	NUCLEOTIDE SEQUENCE.			
RP	MEDLINE=87162490; PubMed=3030813; DOI=10.1016/0014-5793(87)81501-6;			
RX	Forsgren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;			
RA	"Molecular cloning and characterization of a full-length cDNA clone			
RT	for human plasminogen.";			
RL	FEBS Lett. 213:254-260(1987).			
[3]				
RP	NUCLEOTIDE SEQUENCE.			
RA	Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,			
RA	Mitchell D., Robinson J.H.;			
RT	"Expression of recombinant human plasminogen and aglycoplasminogen in			
RT	Hela cells.";			
RT	Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.			
[4]				
RN	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS LYS-57; GLN-133;			
RP	HIS-261; TRP-408; ASN-472; VAL-494 AND TRP-523.			
RA	Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,			
RA	Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;			
RT	"SeattleSNPa, NHBI HL6682 program for genomic applications, UW-			
RT	PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
[5]				
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RP	TISSUE=Kidney;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			

- RA Piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [16]  
 RP PROTEIN SEQUENCE OF 20-810, AND VARIANT ASN-472.  
 RA Sotttrup-Jensen L., Petersen T.E., Magnusson S.;  
 RL Submitted (JUL-1977) to the PIR data bank.  
 RN [17]  
 RP NUCLEOTIDE SEQUENCE OF 292-810.  
 RX MEDLINE=85023311; PubMed=6148961;  
 RA Malinowski D.P., Sadler J.E., Davie E.W.;  
 RT "Characterization of a complementary deoxyribonucleic acid coding for  
 RL human and bovine plasminogen.";  
 RL Biochemistry 23:4243-4250(1984).  
 RN [18]  
 RP PROTEIN SEQUENCE OF 20-100.  
 RX MEDLINE=75093329; PubMed=122932;  
 RA Wiman B., Wallen P.;  
 RT "Structural relationship between 'glutamic acid' and 'lysine' forms of  
 RL human plasminogen and their interaction with the NH2-terminal  
 RT activation peptide as studied by affinity chromatography.";  
 RL Eur. J. Biochem. 50:489-494(1975).  
 RN [19]  
 RP PROTEIN SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810, AND VARIANT  
 RP ASN-472.  
 RA Sotttrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.;  
 RT "The primary structure of human plasminogen.";  
 RL (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);  
 RL Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,  
 RL Raven Press, New York (1978).  
 RN [10]  
 RP PROTEIN SEQUENCE OF 483-604.  
 RX MEDLINE=76043692; PubMed=126863;  
 RA Wiman B., Wallen P.;  
 RT "Amino-acid sequence of the cyanogen-bromide fragment from human  
 RL plasminogen that forms the linkage between the plasmin chains.";  
 RL Eur. J. Biochem. 58:539-547(1975).  
 RN [11]  
 RP PROTEIN SEQUENCE OF 591-810.  
 RX MEDLINE=77225245; PubMed=142009;  
 RA Wiman B.;  
 RT "Primary structure of the B-chain of human plasmin.";  
 RL Eur. J. Biochem. 76:129-137(1977).  
 RN [12]  
 RP ACTIVE SITE.  
 RX MEDLINE=73149248; PubMed=4694729;  
 RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;  
 RT "The primary structure of human plasminogen. II. The histidine loop of  
 RL human plasmin: light (B) chain active center histidine sequence.";  
 RL J. Biol. Chem. 248:1631-1633(1973).  
 RN [13]  
 RP ACTIVE SITE.  
 RX MEDLINE=69234739; PubMed=4240117;  
 RA Groeskopf W.R., Summaria L., Robbins K.C.;  
 RT "Studies on the active center of human plasmin. Partial amino acid  
 RT sequence of a peptide containing the active center serine residue.";  
 RL J. Biol. Chem. 244:3590-3597(1969).  
 RN [14]  
 RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.  
 RX MEDLINE=82213905; PubMed=6919539;  
 RA Trexler M., Vali Z., Patthy L.;  
 RT "Structure of the omega-aminocarboxylic acid-binding sites of human  
 RL plasminogen. Arginine 70 and aspartic acid 56 are essential for  
 RT binding of ligand by kringle 4.";  
 RL J. Biol. Chem. 257:7401-7406(1982).  
 RN [15]  
 RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.  
 RX MEDLINE=85054794; PubMed=6094526;  
 RA Vali Z., Patthy L.;  
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are  
 RT essential for fibrin affinity of the kringle 1 domain.";  
 RL J. Biol. Chem. 259:13690-13694(1984).  
 RN [16]  
 RP PHOSPHORYLATION SITE SER-597.  
 RX MEDLINE=97345939; PubMed=9201958; DOI=10.1021/bi970328d;  
 RA Wang H., Prorok M., Bretthauer R.K., Castellino F.J.;  
 RT "Serine-578 is a major phosphorylation locus in human plasma  
 RL plasminogen.";  
 RL Biochemistry 36:8100-8106(1997).  
 RN [17]  
 RP CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=88185329; PubMed=3356193;  
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,  
 RA Gerwig G.J., van Halbeek H., Vliegenthart J.F.;  
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine  
 RL plasminogen. Species specificity in relation to sialylation and  
 RL fucosylation patterns.";  
 RL Eur. J. Biochem. 173:57-63(1988).  
 RN [18]  
 RP CARBOHYDRATE-LINKAGE SITE SER-268.  
 RX MEDLINE=97207306; PubMed=9054441; DOI=10.1074/jbc.272.11.7408;  
 RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,  
 RA Pizzo S.V.;  
 RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of  
 RL human plasminogen 2.";  
 RL J. Biol. Chem. 272:7408-7411(1997).  
 RN [19]  
 RP CHARACTERIZATION OF ANGIOTATIN, AND PARTIAL PROTEIN SEQUENCE.  
 RX MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;  
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,  
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;  
 RT "Angiotatin: a novel angiogenesis inhibitor that mediates the  
 RL suppression of metastases by a Lewis lung carcinoma.";  
 RL Cell 79:315-328(1994).  
 RN [20]  
 RP CHARACTERIZATION OF ANGIOTATIN.  
 RX MEDLINE=97238710; PubMed=9102221;  
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,  
 RA Lapcevich R., Nacy C.A.;  
 RT "A recombinant human angiotatin protein inhibits experimental primary  
 RL and metastatic cancer.";  
 RL Cancer Res. 57:1329-1334(1997).  
 RN [21]  
 RP INTERACTION WITH CSPG4, AND DOMAIN.  
 RX PubMed=10889192; DOI=10.1074/jbc.M002290200;  
 RA Goretzki L., Lombardo C.R., Stallcup W.B.;  
 RT "Binding of the NC2 proteoglycan to kringle domains modulates the  
 RL functional properties of angiotatin and plasmin(ogen).";  
 RL J. Biol. Chem. 275:28625-28633(2000).  
 RN [22]  
 RP INTERACTION WITH AMOT.  
 RX PubMed=16043488; DOI=10.1074/jbc.M503915200;  
 RA Bratt A., Birot O., Sinha I., Veitonmaeki N., Aase K., Ernkviist M.,  
 RA Holmgren L.;  
 RT "Angiomotin regulates endothelial cell-cell junctions and cell  
 RL motility.";  
 RL J. Biol. Chem. 280:34859-34869(2005).  
 RN [23]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.  
 RX MEDLINE=92031502; PubMed=1657148;  
 RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;  
 RT "Crystal and molecular structure of human plasminogen kringle 4  
 RL refined at 1.9-A resolution.";

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RL Biochemistry 30:10576-10588 (1991).
RL [24]
Query Match 99.7%; Score 1535; DB 1; Length 810;
Best Local Similarity 99.6%; Pred. No. 4.9e-109;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYGTMTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGKNGYGTMTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 157
QY 61 DQGPWCYTTDPEKRYDYCDILCEBECMHCSGENTDGKISKTMSGLECOAWDSQSPHAH 120
DB 158 DQGPWCYTTDPEKRYDYCDILCEBECMHCSGENTDGKISKTMSGLECOAWDSQSPHAH 217
QY 121 GYIPSPFPNKLKKNYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
DB 218 GYIPSPFPNKLKKNYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 277
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 278 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357
RESULT 2
Q5TEH4 HUMAN PRELIMINARY; PRT; 810 AA.
AC Q5TEH4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 8.
DE Plasminogen.
GN Name:PLG; ORFNames=RPI-81D.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AL109933; CAI22908.1; -; Genomic DNA.
DR SMR; Q5TEH4; 562-810.
DR Ensembl; ENSG00000122194; Homo sapiens.
DR GO; GO:005509; F:calcium ion binding; IEA.
DR GO; GO:008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:006508; P:proteolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR011358; Peptidase S1.
DR InterPro; IPR01254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR003966; Peptidase_S1A_pp.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN 1; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001150; plasmin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.

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DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE 1; UNKNOWN_5.
DR PROSITE; PS00070; KRINGLE 2; 5.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS02040; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin SER; 1.
KW Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 810 AA; 90569 MW; 8B31CB877CCB3AB6 CRC64;
Query Match 99.7%; Score 1535; DB 2; Length 810;
Best Local Similarity 99.6%; Pred. No. 4.9e-109;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYGTMTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGKNGYGTMTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 157
QY 61 DQGPWCYTTDPEKRYDYCDILCEBECMHCSGENTDGKISKTMSGLECOAWDSQSPHAH 120
DB 158 DQGPWCYTTDPEKRYDYCDILCEBECMHCSGENTDGKISKTMSGLECOAWDSQSPHAH 217
QY 121 GYIPSPFPNKLKKNYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
DB 218 GYIPSPFPNKLKKNYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 277
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 278 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357
RESULT 3
Q5R8X6 PONPY PRELIMINARY; PRT; 810 AA.
AC Q5R8X6;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DT 07-FEB-2006, entry version 12.
DE Hypothetical protein DKFp470G2422.
GN Names=DKFp470G2422;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Fewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RA Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CR859622; CAH91784.1; -; mRNA.
DR SMR; Q5R8X6; 185-352, 564-810.
DR GO; GO:005509; F:calcium ion binding; IEA.
DR GO; GO:008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:006508; P:proteolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.

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DR InterPro; IPR011358; Pept S1A, Plasmin.
DR InterPro; IPR001254; Peptidase S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pp.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN 1; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001150; Plasmin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
DR PROSITE; PS50070; KRINGLE_2; 5.
DR PROSITE; PS50948; PAN; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Hypothetical protein; Kringle; Protease; Serine protease.
SQ SEQUENCE 810 AA; 90360 MW; 126D530C9942ADD4 CRC64;

Query Match          94.7%; Score 1458; DB 2; Length 810;
Best Local Similarity 95.0%; Pred. No. 3.8e-103;
Matches 247; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRGTMSKTKNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGNYRGTMSKTKNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 157
QY 61 DQGPWCYTTDPEKYDYCDILECEECMHCSENGYDGIKSTMSGLECQAWDSQSPHAX 120
DB 158 DAQGPWCYTTDPEHYDYCDIPECEACMHCSENGYDGIKSTMSGLECQAWDSQSPHAX 217
QY 121 GYIPSKFNKLNKYNCRNPDELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTVQCULK 180
DB 218 GYIPSKFNKLNKYNCRNPDEPRWCFTTDPNKRWELCDIPRCTTPPSSGPTVQCULK 277
QY 181 GTGENYRGNVAVTSGHTCQHSQAQTPHTHTPEFPCKNLDENYCRNPDGKRAPWCHT 240
DB 278 GTGENYRGNVAVTSGHTCQHSQAQTPHTHTPEFPCKNLDENYCRNPDGKAPWCYT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCGSSPV 357

RESULT 4
ID PLMN MACMU STANDARD; PRT; 810 AA.
AC P12545;
DT 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1989, sequence version 1.
DT 07-MAR-2006, entry version 65.
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;
DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
DE chain B].
GN Name=PLG;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]_
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=89174660; PubMed=2925643;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
RT synthesis."
RL J. Biol. Chem. 264:5957-5965(1989).
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as

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a proteolytic factor in a variety of other processes including
embryonic development, tissue remodeling, tumor invasion, and
inflammation; in ovulation it weakens the walls of the Graafian
follicle. It activates the urokinase-type plasminogen activator,
collagenases and several complement zymogens, such as C1 and C5.
It cleaves fibrin, fibronectin, thrombospondin, laminin and von
Willebrand factor. Its role in tissue remodeling and tumor
invasion may be modulated by CSPG4.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
products.
-!- ENZYME REGULATION: Converted into plasmin by plasminogen
activators, both plasminogen and its activator being bound to
fibrin. Activated with catalytic amounts of streptokinase.
-!- SUBUNIT: Interacts with CSPG4 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted protein.
-!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By
similarity).
-!- PTM: In the presence of the inhibitor, the activation involves
only cleavage after Arg-580, yielding two chains held together by
two disulfide bonds. In the absence of the inhibitor, the
activation involves additionally the removal of the activation
peptide (By similarity).
-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
immediately after dissociation from the clot.
-!- MISCELLANEOUS: In the presence of the inhibitor, the activation
involves only cleavage after Arg-580, resulting in 2 chains held
together by 2 disulfide bonds. Without the inhibitor, the
activation involves also removal of the activation peptide.
-!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
subfamily.
-!- SIMILARITY: Contains 5 kringle domains.
-!- SIMILARITY: Contains 1 PAN domain.
-!- SIMILARITY: Contains 1 peptidase S1 domain.
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EMBL; J04697; AAA36901.1; -; mRNA.
PIR; B32869; B30848.
HSSP; P00747; 1BUI.
SMR; P12545; 184-352, 564-810.
MEROPS; S01.233; -.
LinkHub; P12545; -.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan app.
InterPro; IPR011358; Pept S1A, Plasmin.
InterPro; IPR001254; Peptidase S1_S6.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR003966; Peptidase_S1A_pp.
Pfam; PF00051; Kringle; 5.
Pfam; PF00024; PAN 1; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001150; Plasmin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 5.
SMART; SM00130; KR; 5.
SMART; SM00473; PAN AP; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50948; PAN; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;
RT Signal
FT SIGNAL 1 19
FT CHAIN 20 810 Plasminogen.
FT /FTID=PRO_0000028059.

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```
FT CHAIN 20 580 Plasmin heavy chain A.
FT PEPTIDE 20 96 /FTid=PRO_0000028060.
FT 20 96 Activation peptide.
FT CHAIN 97 580 /FTid=PRO_0000028061.
FT 97 580 Plasmin heavy chain A, short form.
FT CHAIN 581 810 /FTid=PRO_0000028062.
FT 581 810 Plasmin light chain B.
FT 581 810 /FTid=PRO_0000028063.
FT DOMAIN 20 98 PAN.
FT DOMAIN 103 181 Kringle 1.
FT DOMAIN 184 262 Kringle 2.
FT DOMAIN 275 352 Kringle 3.
FT DOMAIN 377 454 Kringle 4.
FT DOMAIN 481 560 Kringle 5.
FT DOMAIN 581 808 Peptidase S1.
FT ACT_SITE 622 622 Charge relay system.
FT ACT_SITE 665 665 Charge relay system.
FT ACT_SITE 760 760 Charge relay system.
FT BINDING 134 134 Fibrin.
FT BINDING 136 136 Fibrin.
FT BINDING 136 136 Omega-aminocarboxylic acids.
FT BINDING 158 158 Omega-aminocarboxylic acids.
FT BINDING 172 172 Omega-aminocarboxylic acids.
FT BINDING 432 432 Omega-aminocarboxylic acids.
FT BINDING 445 445 Omega-aminocarboxylic acids.
FT CARBOHYD 365 365 O-linked (GalNAc...) (By similarity).
FT DISULFID 49 73 By similarity.
FT DISULFID 53 61 By similarity.
FT DISULFID 103 181 By similarity.
FT DISULFID 124 164 By similarity.
FT DISULFID 152 176 By similarity.
FT DISULFID 185 262 By similarity.
FT DISULFID 188 316 By similarity.
FT DISULFID 206 245 By similarity.
FT DISULFID 234 257 By similarity.
FT DISULFID 275 352 By similarity.
FT DISULFID 296 335 By similarity.
FT DISULFID 324 347 By similarity.
FT DISULFID 377 454 By similarity.
FT DISULFID 398 437 By similarity.
FT DISULFID 426 449 By similarity.
FT DISULFID 481 560 By similarity.
FT DISULFID 502 543 By similarity.
FT DISULFID 531 555 By similarity.
FT DISULFID 567 685 Interchain (between A and B chains) (By similarity).
FT 577 585 Interchain (between A and B chains) (By similarity).
FT 607 623 By similarity.
FT DISULFID 699 766 By similarity.
FT DISULFID 729 745 By similarity.
FT DISULFID 756 784 By similarity.
SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A1A0F24A CRC64;

Query Match 93.6%; Score 1442; DB 1; Length 810;
Best Local Similarity 93.1%; Pred. NO. 6.4e-102;
Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKMTGKNGITCQKWSSTSPHRPFSPTHPSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGNYRTGKMTGKNGITCQKWSSTSPHRPFSPTHPSEGLEENYCRNPDN 157
QY 61 DPQGPWCYTTDPEKRYDYCDILECEECMHCSENGYDGKISKTMSGLECQAWDSQSPFAH 120
DB 158 DGQGPWCYTTDPEERPDYCDIPECEDECMHCSENGYDGKISKTMSGLECQAWDSQSPFAH 217
QY 121 GYIPSKFPNNLKQNYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTTPPPSGPTTQCLK 180
DB 218 GYIPSKFPNNLKQNYCRNPDRGEPPEPWCFTTDPNKRWELCDIPRCTTTPPPSGPTTQCLK 277
QY 181 GTGNYRGNAVTVSGHTCOHWSAQTPHTHTPENFPCKNLNDENYCRNPDKGRAPWCHT 240
DB 278 GTGNYRGNAVTVSGHTCHGWSAQTPHTHTPENFPCKNLNDENYCRNPDKGRAPWCHT 337
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QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 5
Q8WNR1 CANFA
ID Q8WNR1 CANFA PRELIMINARY; PRT; 359 AA.
AC Q8WNR1;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Plasminogen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Pirie-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
RA Folkman J., Waters D.J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
EMBL; AY069985; AAL58519.1; -; mRNA.
DR HSSP; P00747; 1PMK.
DR SMR; Q8WNR1; 87-255.
DR Ensembl; ENSCARG0000000759; Canis familiaris.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Peptidase_S1A_pp.
DR Pfam; PF00051; Kringle; 4.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KB; 4.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PSS0070; KRINGLE_2; 4.
DR Kring.
DR Kring.
FT NON_TER 1 1
FT NON_TER 359 359
SQ SEQUENCE 359 AA; 41173 MW; 776D35F4AB0BDD9E CRC64;

Query Match 84.8%; Score 1306; DB 2; Length 359;
Best Local Similarity 81.2%; Pred. NO. 6.9e-92;
Matches 211; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKMTGKNGITCQKWSSTSPHRPFSPTHPSEGLEENYCRNPDN 60
DB 1 IYLSECKTGNGTYRTGKMTGKNDVACQKWSNPHKPNYTPKHPLEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPEKRYDYCDILECEECMHCSENGYDGKISKTMSGLECQAWDSQSPFAH 120
DB 61 DENGWPCTTNDVDFDYCDIPECEDECMHCSENGYDGKISKTMSGLECQAWDSQSPFAH 120
QY 121 GYIPSKFPNNLKQNYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTTPPPSGPTTQCLK 180
DB 121 GYIPSKFPNNLKQNYCRNPDRGEPPEPWCFTTDPNKRWELCDIPRCTTTPPPSGPTTQCLK 180
QY 181 GTGNYRGNAVTVSGHTCOHWSAQTPHTHTPENFPCKNLNDENYCRNPDKGRAPWCHT 240
DB 181 GRGESYRGKSVTVSGHTCOHWSAQTPHTHTPENFPCKNLNDENYCRNPDKGRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 357
```

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RESULT 6  
PLMN\_RAT  
ID PLMN RAT STANDARD; PRT; 812 AA.  
AC Q01177; Q9ROW3;  
DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.  
DT 31-AUG-2004, sequence version 2.  
DT 07-WAR-2006, entry version 50.  
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;  
DE Activation peptide; Angiostatin; Plasmin heavy chain A, short form;  
DE Plasmin light chain B].  
GN Name=Plg;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]  
RN NUCLEOTIDE SEQUENCE [MRNA].  
RP NUCLEOTIDE SEQUENCE [MRNA] OF 343-511.  
RC TISSUE=Liver;  
RA Bangert K., Johnsen A.H., Thorsen S.;  
RT "Rat plasminogen: cDNA and gene structure.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
[2]  
RN NUCLEOTIDE SEQUENCE [MRNA] OF 343-511.  
RC TISSUE=Liver;  
RX MEDLINE=91250378; PubMed=1645711;  
RA Kanalas J.J., Makker S.P.;  
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a  
RT receptor site for plasminogen.";  
RL J. Biol. Chem. 266:10825-10829 (1991).  
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
CC a proteolytic factor in a variety of other processes including  
CC embryonic development, tissue remodeling, tumor invasion, and  
CC inflammation; in ovulation it weakens the walls of the Graafian  
CC follicle. It activates the urokinase-type plasminogen activator,  
CC collagenases and several complement zymogens, such as C1 and C5.  
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von  
CC Willebrand factor. Its role in tissue remodeling and tumor  
CC invasion may be modulated by CSPG4.  
CC -!- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks  
CC neovascularization and growth of experimental primary and  
CC metastatic tumors in vivo (By similarity). Lys-|-Xaa > Arg-|-Xaa;  
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;  
CC higher selectivity than trypsin. Converts fibrin into soluble  
CC products.  
CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen  
CC activators, both plasminogen and its activator being bound to  
CC fibrin. Cannot be activated with streptokinase.  
CC -!- SUBUNIT: Interacts with CSPG4 and AMO1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted protein.  
CC -!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By  
CC similarity).  
CC -!- PTM: In the presence of the inhibitor, the activation involves  
CC only cleavage after Arg-581, yielding two chains held together by  
CC two disulfide bonds. In the absence of the inhibitor, the  
CC activation involves additionally the removal of the activation  
CC peptide (By similarity).  
CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin  
CC immediately after dissociation from the clot.  
CC -!- MISCELLANEOUS: In the presence of the inhibitor, the activation  
CC involves only cleavage after Arg-581, resulting in 2 chains held  
CC together by 2 disulfide bonds. Without the inhibitor, the  
CC activation involves also removal of the activation peptide (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
CC subfamily.  
CC -!- SIMILARITY: Contains 5 kringle domains.  
CC -!- SIMILARITY: Contains 1 PAN domain.  
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC  
CC  
DR EMBL; AJ242649; CAB46014.1; -, mRNA.  
DR EMBL; M62832; AAA41884.1; -, mRNA.  
DR PIR; A40522; A40522.  
DR HSP; P00747; IPMK.  
DR SMR; Q01177; 565-812.  
DR MEROPS; S01.233; -.  
DR Ensembl; ENSRNOG0000017223; Rattus norvegicus.  
DR RGD; 619893; Plg.  
DR InterPro; IPR000001; Kringle.  
DR InterPro; IPR003014; PAN.  
DR InterPro; IPR003609; Pan\_app.  
DR InterPro; IPR011358; Pept\_S1A\_Plasmin.  
DR InterPro; IPR001254; Peptidase\_S1\_S6.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR003966; Peptidase\_S1A\_pp.  
DR Pfam; PF00051; Kringle; 5.  
DR Pfam; PF00024; PAN 1; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001150; Plasmin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; KRINGLE.  
DR PRINTS; PR01505; PROTHROMBIN.  
DR ProDom; PD000395; Kringle; 1.  
DR SMART; SM00130; KR; 5.  
DR SMART; SM00473; PAN\_AP; 1.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00021; KRINGLE\_1; 5.  
DR PROSITE; PS00070; KRINGLE\_2; 5.  
DR PROSITE; PS00948; PAN; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Blood coagulation; Fibrinolysis; Hydrolase; Kringle; Protease; Repeat;  
KW Serine protease; Signal; Tissue remodeling; Zymogen.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 812 Plasminogen.  
FT CHAIN 20 581 Plasmin heavy chain A.  
FT PEPTIDE 20 97 /FTID=PRO\_0000028080.  
FT CHAIN 98 581 Activation peptide (By similarity).  
FT CHAIN 98 581 /FTID=PRO\_0000028081.  
FT CHAIN 98 581 Plasmin heavy chain A, short form.  
FT CHAIN 98 581 /FTID=PRO\_0000028082.  
FT CHAIN 582 812 Angiostatin.  
FT CHAIN 582 812 /FTID=PRO\_0000028083.  
FT CHAIN 582 812 Plasmin light chain B.  
FT CHAIN 582 812 /FTID=PRO\_0000028084.  
FT DOMAIN 20 98 PAN.  
FT DOMAIN 102 181 Kringle 1.  
FT DOMAIN 184 262 Kringle 2.  
FT DOMAIN 274 352 Kringle 3.  
FT DOMAIN 375 454 Kringle 4.  
FT DOMAIN 480 560 Kringle 5.  
FT DOMAIN 582 810 Peptidase S1.  
FT ACT\_SITE 624 824 Charge relay system (By similarity).  
FT ACT\_SITE 667 762 Charge relay system (By similarity).  
FT ACT\_SITE 762 762 Charge relay system (By similarity).  
FT DISULFID 49 73 By similarity.  
FT DISULFID 53 61 By similarity.  
FT DISULFID 103 181 By similarity.  
FT DISULFID 124 164 By similarity.  
FT DISULFID 152 176 By similarity.  
FT DISULFID 185 262 By similarity.  
FT DISULFID 188 316 By similarity.  
FT DISULFID 206 245 By similarity.  
FT DISULFID 234 257 By similarity.  
FT DISULFID 275 352 By similarity.  
FT DISULFID 296 335 By similarity.  
FT DISULFID 324 347 By similarity.  
FT DISULFID 376 454 By similarity.  
FT DISULFID 397 437 By similarity.

FT DISULFID 425 449 By similarity.  
 FT DISULFID 481 560 By similarity.  
 FT DISULFID 502 543 By similarity.  
 FT DISULFID 531 555 By similarity.  
 FT DISULFID 568 687 Interchain (between A and B chains) (By similarity)  
 FT DISULFID 578 586 Interchain (between A and B chains) (By similarity)  
 FT DISULFID 609 625 By similarity.  
 FT DISULFID 701 768 By similarity.  
 FT DISULFID 731 747 By similarity.  
 FT DISULFID 758 786 By similarity.  
 FT CONFLICT 418 418 A -> S (in Ref. 2).  
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410EBC9E CRC64;

Query Match 84.4%; Score 1299; DB 1; Length 812;  
 Best Local Similarity 82.6%; Pred. No. 5.8e-91;  
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
 Db 98 VYLSECKTGNGNYRTGKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DPQGPWCYTTPDEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLCQAWDSQSPHAF 120  
 Db 158 DRQGPWCYTTPDQRYEYCNIPCEBECMHCSENGYDGIKSKTMSGLCQAWDSQSPHAF 217

QY 121 GYIPSKFPNNLKNYCRNPDRELPRWCFTTDPNKRWEICDIPRCTTTPPPSGTTCCLK 180  
 Db 218 GYIPAKFPNNLKNYCRNPDRELPRWCFTTDPNKRWEICDIPRCTTTPPPSGTTCCLK 277

QY 181 GTGNYRGVNAVTVSGHTCQHWSAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
 Db 278 GRGNYRGVNAVTVSGHTCQHWSAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVREYCKIPSCDSS 258  
 Db 338 TDSQLRWEYCEIPSCSS 355

RESULT 7  
 Q5BK6 RAT PRELIMINARY; PRT; 812 AA.  
 AC Q5BK6;  
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Plasminogen.  
 GN Name:Plg;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ushin T.B., Toehiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fackey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RESULT 8

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
 RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RG NIH MGC Project;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 CC EMBL; BC091135; AAH91135.1; -; mRNA.  
 DR SMR; Q5BK6; 565-812.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004283; F:plasmin activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR GO; GO:0050874; P:organismal physiological process; IEA.  
 DR GO; GO:0008508; P:proteolysis; IEA.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan app.  
 DR InterPro; IPR011358; Pept\_SIA\_Plasmin.  
 DR InterPro; IPR01254; Peptidase\_S1\_S6.  
 DR InterPro; IPR01314; Peptidase\_S1A.  
 DR InterPro; IPR003966; Peptidase\_S1A\_pp.  
 DR Pfam; PF00051; Kringle; 5.  
 DR Pfam; PF00024; PAN 1; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PIRSF; PIRSF001150; Plasmin; 1.  
 DR PRINTS; PRO00722; CHYMOTRYPSIN.  
 DR PRINTS; PRO0018; KRINGLE.  
 DR PRINTS; SM01505; PROTHROMBIN.  
 DR SMART; SM00130; KR; 5.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; UNKNOWN\_5.  
 DR PROSITE; PS50070; KRINGLE\_2; 5.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Kringle; Protease; Serine protease.  
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410EBC9E CRC64;

Query Match 84.4%; Score 1299; DB 2; Length 812;  
 Best Local Similarity 82.6%; Pred. No. 5.8e-91;  
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
 Db 98 VYLSECKTGNGNYRTGKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DPQGPWCYTTPDEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLCQAWDSQSPHAF 120  
 Db 158 DRQGPWCYTTPDQRYEYCNIPCEBECMHCSENGYDGIKSKTMSGLCQAWDSQSPHAF 217

QY 121 GYIPSKFPNNLKNYCRNPDRELPRWCFTTDPNKRWEICDIPRCTTTPPPSGTTCCLK 180  
 Db 218 GYIPAKFPNNLKNYCRNPDRELPRWCFTTDPNKRWEICDIPRCTTTPPPSGTTCCLK 277

QY 181 GTGNYRGVNAVTVSGHTCQHWSAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
 Db 278 GRGNYRGVNAVTVSGHTCQHWSAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVREYCKIPSCDSS 258  
 Db 338 TDSQLRWEYCEIPSCSS 355



PLMN\_PIG  
 ID PLMN\_PIG STANDARD; PRT; 790 AA.  
 AC P06867;  
 DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.  
 DT 01-FEB-1991, entry version 2.  
 DT 07-MAR-2006, entry version 66.  
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;  
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light  
 DE chain B].  
 GN Name=PLG;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 OC Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP PROTEIN SEQUENCE OF 1-560.  
 RA Schaller J., Marti T., Roessel S.J., Kaempfer U., Rickli E.E.;  
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison  
 RT of the carbohydrate attachment sites with the human and bovine  
 RT species.";  
 RL Fibrinolysis 1:91-102(1987).  
 RN [2]  
 RP PROTEIN SEQUENCE OF 450-790.  
 RX MEDLINE=85203907; PubMed=3846533;  
 RA Marti T., Schaller J., Rickli E.E.;  
 RT "Determination of the complete amino-acid sequence of porcine  
 RT miniplasminogen.";  
 RL Eur. J. Biochem. 149:279-285(1985).  
 RN [3]  
 RP CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=88185329; PubMed=3356193;  
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,  
 RA Gerwig G.J., van Halbeek H., Vliegthart J.F.;  
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine  
 RT plasminogen. Species specificity in relation to sialylation and  
 RT fucosylation patterns.";  
 RL Eur. J. Biochem. 173:57-63(1988).  
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenases and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von  
 CC Willebrand factor. Its role in tissue remodeling and tumor  
 CC invasion may be modulated by CSPG4.  
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-[Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen  
 CC activators, both plasminogen and its activator being bound to  
 CC fibrin. Cannot be activated with streptokinase.  
 CC -!- SUBUNIT: Interacts with CSPG4 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted protein.  
 CC -!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By  
 CC similarity).  
 CC -!- PTM: N-linked glycan contains N-acetylglucosamine, sialic acid and  
 CC is core fucosylated. O-linked glycans consist of Gal-GalNAc  
 CC disaccharide which is modified with up to 2 sialic acid residues  
 CC (microheterogeneity).  
 CC -!- PTM: In the presence of the inhibitor, the activation involves  
 CC only cleavage after Arg-560, yielding two chains held together by  
 CC two disulfide bonds. In the absence of the inhibitor, the  
 CC activation involves additionally the removal of the activation  
 CC peptide (By similarity).  
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin  
 CC immediately after dissociation from the clot.  
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 5 kringle domains.  
 CC -!- SIMILARITY: Contains 1 PAN domain.  
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.

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 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC -----  
 CC PIR; S03733; PLPG.  
 DR HSSP; P00747; 1BUI.  
 DR SMR; P06867; 544-790.  
 DR MEROPS; S01.233; -.  
 DR GlycoSuiteDB; P06867; -.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan app.  
 DR InterPro; IPR011358; Pept\_S1A\_Plasmin.  
 DR InterPro; IPR001354; Peptidase\_S1\_S6.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR003966; Peptidase\_S1A\_pp.  
 DR Pfam; PF00051; Kringle; 5.  
 DR Pfam; PF00024; PAN 1; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PIRSF; PIRSF001150; Plasmin; 1.  
 DR PRINTS; PRO0722; CHYMOTRYPSIN.  
 DR PRINTS; PRO0018; KRINGLE.  
 DR PRINTS; PRO1505; PROTHROMBIN.  
 DR ProDom; PD000395; Kringle; 5.  
 DR SMART; SM00130; KR; 5.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 5.  
 DR PROSITE; PS00070; KRINGLE\_2; 5.  
 DR PROSITE; PS00948; PAN; 1.  
 DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Direct protein sequencing; Fibrinolysis;  
 KW Glycoprotein; Hydrolase; Kringle; Protease; Repeat; Serine protease;  
 KW Tissue remodeling; Zymogen.  
 FT CHAIN 1 560 Plasmin heavy chain A.  
 FT PEPTIDE 1 78 /FTID=PRO\_0000028075.  
 FT CHAIN 79 560 Activation peptide (By similarity).  
 FT CHAIN 560 /FTID=PRO\_0000028076.  
 FT CHAIN 561 790 Plasmin heavy chain A, short form.  
 FT CHAIN 561 790 /FTID=PRO\_0000028077.  
 FT CHAIN 561 790 Plasmin light chain B.  
 FT CHAIN 561 790 /FTID=PRO\_0000028078.  
 FT DOMAIN 1 79 PAN.  
 FT DOMAIN 84 162 Kringle 1.  
 FT DOMAIN 166 243 Kringle 2.  
 FT DOMAIN 256 333 Kringle 3.  
 FT DOMAIN 358 435 Kringle 4.  
 FT DOMAIN 461 540 Kringle 5.  
 FT DOMAIN 561 788 Peptidase S1.  
 FT ACT\_SITE 602 602 Charge relay system.  
 FT ACT\_SITE 645 645 Charge relay system.  
 FT ACT\_SITE 740 740 Charge relay system.  
 FT CARBOHYD 289 289 N-linked (GlcNAc...).  
 FT CARBOHYD 340 340 /FTID=CAR\_000019.  
 FT DISULFID 30 54 O-linked (GalNAc...).  
 FT DISULFID 34 42 /FTID=CAR\_000020.  
 FT DISULFID 84 162 By similarity.  
 FT DISULFID 105 145 By similarity.  
 FT DISULFID 133 157 By similarity.  
 FT DISULFID 166 243 By similarity.  
 FT DISULFID 169 297 By similarity.  
 FT DISULFID 187 226 By similarity.  
 FT DISULFID 215 238 By similarity.  
 FT DISULFID 256 333 By similarity.  
 FT DISULFID 277 316 By similarity.  
 FT DISULFID 305 328 By similarity.  
 FT DISULFID 358 435 By similarity.  
 FT DISULFID 379 418 By similarity.  
 FT DISULFID 407 430 By similarity.







RESULT 11

PLNM	MOUSE	STANDARD;	PRT;	812 AA.
ID	PLNM	MOUSE		
AC	P20918;	Q8CIS2;	Q91WJ5;	
DT	01-FEB-1991,	integrated into	UniProtKB/Swiss-Prot.	
DT	30-MAY-2003,	sequence version 2.		
DT	07-MAR-2006,	entry version 76.		
DE	Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;			
DE	Activation peptide; Angiostatatin; Plasmin heavy chain A, short form;			
DE	Plasmin light chain B].			
GN	Name=Plg;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	[1]			
RP	NCLEOTIDE SEQUENCE.			
RP	MEDLINE=91184812; PubMed=2081600;			
RP	Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;			
RP	"Characterization of the cDNA coding for mouse plasminogen and			
RP	localization of the gene to mouse chromosome 17.";			
RP	Genomics 8:49-61(1990).			
RP	[2]			
RP	NCLEOTIDE SEQUENCE.			
RP	STRAIN=129/Sv;			
RP	Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,			
RP	Nagaraja R.;			
RP	"Genomic sequence analysis in the mouse t-complex region.";			
RP	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
RP	[3]			
RP	NCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RP	TISSUE=Liver;			
RP	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;			
RP	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RP	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RP	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,			
RP	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RP	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RP	Stapleton M., Soares M.B., Bonaldo M.F., Casavent T.I., Scheetz T.E.,			
RP	Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RP	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RP	Resak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RP	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RP	Villañola D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RP	Fahy J., Hulton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,			
RP	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE OF 1-16.  
 RP STRAIN=129/SVJ; TISSUE=Liver;  
 RC MEDLINE=2254943; PubMed=12149246; DOI=10.1074/jbc.M202509200;  
 RX Bannach P.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,  
 RA Parmer R.J., Miles L.A.;  
 RA "Localization of regulatory elements mediating constitutive and  
 RT cytokine-stimulated plasminogen gene expression".  
 RL J. Biol. Chem. 277:38579-38588 (2002).  
 RN [5]  
 RN CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE  
 RP MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;  
 RX O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,  
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;  
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the  
 RT suppression of metastases by a Lewis lung carcinoma.";  
 RL Cell 79:315-328 (1994).  
 RN CC  
 CC -I- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenases and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von  
 CC Willebrand factor. Its role in tissue remodeling and tumor  
 CC invasion may be modulated by CSPG4.  
 CC -I- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks  
 CC neovascularization and growth of experimental primary and  
 CC metastatic tumors in vivo.  
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -I- ENZYME REGULATION: Converted into plasmin by plasminogen  
 CC activators, both plasminogen and its activator being bound to  
 CC fibrin. Cannot be activated with streptokinase.  
 CC -I- SUBUNIT: Interacts with CSPG4 and AMOT (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Secreted protein.  
 CC -I- DOMAIN: Kringle domains mediate interaction with CSPG4 (By  
 CC similarity).  
 CC -I- PTM: In the presence of the inhibitor, the activation involves  
 CC only cleavage after Arg-581, yielding two chains held together by  
 CC two disulfide bonds. In the absence of the inhibitor, the  
 CC activation involves additionally the removal of the activation  
 CC peptide (By similarity).  
 CC -I- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin  
 CC immediately after dissociation from the clot.  
 CC -I- MISCELLANEOUS: In the presence of the inhibitor, the activation  
 CC involves only cleavage after Arg-581, resulting in 2 chains held  
 CC together by 2 disulfide bonds. Without the inhibitor, the  
 CC activation involves also removal of the activation peptide.  
 CC -I- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
 CC subfamily.  
 CC -I- SIMILARITY: Contains 5 kringle domains.  
 CC -I- SIMILARITY: Contains 1 PAN domain.  
 CC -I- SIMILARITY: Contains 1 peptidase S1 domain.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs license  
 CC  
 CC ENBL; J04766; AAA50168.1; -; mRNA.  
 DR ENBL; AF481053; AAM22156.1; -; Genomic\_DNA.  
 DR ENBL; BC014773; AAH14773.1; -; mRNA.  
 DR ENBL; BC057186; AAH57186.1; -; mRNA.  
 DR ENBL; AY134430; AAN15805.1; -; Genomic\_DNA.  
 DR PIR; A38514; P1MS.  
 DR HSSP; P00747; 1BU1.

DR PIR, P20918; 566-812.  
DR MEROPS; S01.233; -.  
DR Ensembl; ENSMUSG0000059481; Mus musculus.  
DR MGI; MGI:97620; P19.  
DR GO; GO:0003615; C:extracellular space; TAS.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR GO; GO:0006917; P:induction of apoptosis; IDA.  
DR GO; GO:0046716; P:muscle maintenance; IMP.  
DR GO; GO:0045445; P:myoblast differentiation; IMP.  
DR GO; GO:0016525; P:negative regulation of angiogenesis; TAS.  
DR GO; GO:0042246; P:tissue regeneration; IMP.  
DR InterPro; IPR000001; Kringle.  
DR InterPro; IPR003014; PAN.  
DR InterPro; IPR003609; Pan\_app.  
DR InterPro; IPR011358; Pept\_S1A\_plasmin.  
DR InterPro; IPR001254; Peptidase\_S1\_S6.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR001366; Peptidase\_S1A\_pp.  
DR Pfam; PF00051; Kringle; 5.  
DR Pfam; PF00024; PAN 1; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001150; Plasmin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; KRINGLE.  
DR PRINTS; PR01505; PROTHROMBIN.  
DR ProDom; PD000395; Kringle; 5.  
DR SMART; SM00130; KR; 5.  
DR SMART; SM00473; PAN\_AP; 1.  
DR SMART; SM00020; TRYPSIN; 1.  
DR PROSITE; PS00021; KRINGLE 1; 5.  
DR PROSITE; PS00070; KRINGLE\_2; 5.  
DR PROSITE; PS00948; PAN; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_SER; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Blood coagulation; Direct protein sequencing; Fibrinolysis; Hydrolase;  
KW Kringle; Protease; Repeat; Serine protease; Signal; Tissue remodeling;  
KW Zymogen.  
FT SIGNAL 1 19  
FT CHAIN 20 812 Plasminogen.  
FT FT /FTid-PRO 0000028069.  
FT CHAIN 20 581 Plasmin heavy chain A.  
FT FT /FTid-PRO 0000028070.  
FT PEPTIDE 20 97 Activation peptide.  
FT FT /FTid-PRO 0000028071.  
FT CHAIN 98 581 Plasmin heavy chain A, short form.  
FT FT /FTid-PRO 0000028072.  
FT CHAIN 98 7436 Angiotensin.  
FT FT /FTid-PRO 0000028073.  
FT CHAIN 582 812 Plasmin light chain B.  
FT FT /FTid-PRO 0000028074.  
FT FT PAN.  
FT DOMAIN 20 98  
FT DOMAIN 103 181 Kringle 1.  
FT DOMAIN 184 262 Kringle 2.  
FT DOMAIN 275 352 Kringle 3.  
FT DOMAIN 377 454 Kringle 4.  
FT DOMAIN 481 560 Kringle 5.  
FT DOMAIN 582 810 Peptidase S1.  
FT ACT SITE 624 624 Charge relay system (By similarity).  
FT ACT SITE 667 667 Charge relay system (By similarity).  
FT ACT SITE 762 762 Charge relay system (By similarity).  
FT DISULFID 49 73 By similarity.  
FT DISULFID 53 61 By similarity.  
FT DISULFID 103 181 By similarity.  
FT DISULFID 124 164 By similarity.  
FT DISULFID 152 176 By similarity.  
FT DISULFID 185 262 By similarity.  
FT DISULFID 188 316 By similarity.  
FT DISULFID 206 245 By similarity.  
FT DISULFID 234 257 By similarity.  
FT DISULFID 275 352 By similarity.  
FT DISULFID 296 335 By similarity.  
FT DISULFID 324 347 By similarity.

FT DISULFID 377 454 By similarity.  
FT DISULFID 398 437 By similarity.  
FT DISULFID 426 449 By similarity.  
FT DISULFID 481 560 By similarity.  
FT DISULFID 502 543 By similarity.  
FT DISULFID 531 555 By similarity.  
FT DISULFID 568 687 Interchain (between A and B chains) (By similarity).  
FT DISULFID 578 586 Interchain (between A and B chains) (By similarity).  
Query Match 83.1%; Score 1279; DB 1; Length 812;  
Best Local Similarity 81.0%; Pred. No. 2e-89;  
Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKVRGTMSTKNGITCKWSTSRPRFSPATHPSSEGLEENYCRNPON 60  
DB 98 VYLSECKTGNGYRGTSRTKSGVACQKRGATFFPHVNPYSTHPNEGLEENYCRNPON 157  
QY 61 DPQGPWCYTTDPKRYDYCDILLECEECWCHSGENYDGRKISKTMSGLECQAWDSQSPHAA 120  
DB 158 DEQGPWCYTTDPKRYDYCNIPCECEECWCHSGENYDGRKISKTMSGLECQAWDSQSPHAA 217  
QY 121 GYIPSKPNKMLKQNYCRNPDRLEPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTVQCLK 180  
DB 218 GYIPAKFPSPKMLKQNYCRNPDEPRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTVQCLK 277  
QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHTHRTPEFCKNLDENYCRNPDKGRAPWCHT 240  
DB 278 GRGENYRGTVSVTVSGKTCQRMSEQTTPHNNHTPFPCKNLEENYCRNPDPGETAPWCYT 337  
QY 241 TNSQVRWEYCKIPSCDSS 258  
DB 338 TDSQLRWEYCEIPSCSS 355  
RESULT 12  
Q3VIT9 MOUSE  
ID Q3VIT9 MOUSE PRELIMINARY; PRT; 812 AA.  
AC Q3VIT9  
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
DT 11-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 6.  
DE 18 days pregnant adult female placenta and extra embryonic tissue  
DE cDNA, RIKEN full-length enriched library, clone:3830402P08  
DE product:plasminogen, full insert sequence.  
GN Name=P19;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Allen J.E.,  
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E.,

RA Gustinich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Huminecki L., Iacono M., Ikeo K., Iwana A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelson J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Supta E., Suglura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.

RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563 (2005).  
 RN [3]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
 RX PubMed16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566 (2005).  
 RN [4]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [5]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [6]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [7]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
 RX MEDLINE=2030913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [8]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;  
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL; AK132254; BAE21060.1; -; mRNA.  
 DR MGI; MGI:97620; Plg.  
 DR GO; GO:0005576; C:extracellular region; RCA.  
 DR GO; GO:0003179; F:hormone activity; RCA.  
 DR GO; GO:0006915; P:apoptosis; IDA.  
 DR GO; GO:0006917; P:induction of apoptosis; IDA.  
 DR GO; GO:0046716; P:muscle maintenance; IMP.  
 DR GO; GO:0045445; P:myoblast differentiation; IMP.  
 DR GO; GO:0016525; P:negative regulation of angiogenesis; TAS.  
 DR GO; GO:0042246; P:tissue regeneration; IMP.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan app.  
 DR InterPro; IPR011358; Pept SIA plasmin.  
 DR InterPro; IPR001254; Peptidase S1 S6.  
 DR InterPro; IPR001314; Peptidase\_S1A.

DR InterPro; IPR003966; Peptidase\_S1A\_pp.

DR Pfam; PF00051; Kringle; 5.

DR Pfam; PF00024; PAN\_1; 1.

DR Pfam; PF00089; Trypsin; 1.

DR PIRSF; PIRSF001150; Plasmin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.

DR PRINTS; PRO0018; KRINGLE.

DR PRINTS; PRO1505; PROTHROMBIN.

DR ProDom; PD000395; Kringle; 5.

DR SMART; SM00130; KR; 5.

DR SMART; SM00473; PAN\_AP; 1.

DR SMART; SM00020; TRYPSIN; 1.

DR PROSITE; PS00021; KRINGLE\_1; 5.

DR PROSITE; PS00070; KRINGLE\_2; 5.

DR PROSITE; PS00948; PAN; 1.

DR PROSITE; PS0240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

#### Query Match

Best Local Similarity 83.1%; Score 1279; DB 2; Length 812;

Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLENYCRNPDPN 60

Db 98 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLENYCRNPDPN 157

QY 61 DPQGPWCYTTPDEKRYDYCDILCEBECMHCNGENYDGIKSTMSGLEQAWDSQSPHAX 120

Db 158 DRQGPWCYTTPDKRYDYCNIPCEBECMYCSEKYEKISKSTMSGLDQAWDSQSPHAX 217

QY 121 GYIPSPKPNKLKKNYCRNPDRRLRPWCFTTDPNKRWELCDIPRCTTPPSSGPTVQCLK 180

Db 218 GYIPAKFPNNLKNYCRNPDRGPRWCFTTDPNKRWELCDIPRCTTPPSSGPTVQCLK 277

QY 181 GTGENYRGNVAVTVSGHTCQHSQAQTPHTERTPENFPCKNLNDENYCRNPDGKRAPWCYT 240

Db 278 GRGENYRGVTVSGTKQKWSSTSPHRPRFSPATHPSEGLENYCRNPDPN 337

QY 241 TNSQVWEYCKIPSCDSS 258

Db 338 TDSQVWEYCKIPSCSS 355

#### RESULT 13

PLMN ERIEU

AC Q29485; STANDARD; PRT; 810 AA.

DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1997, sequence version 1.

DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;

DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light

DE chain B].

CN Name=PLG;

OS Eriaceae europaeus (Western European hedgehog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;

OC Erinaceinae; Erinaceus.

OX NCBI\_TaxID=9365;

RN [1]\_TaxID=9365;

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Liver;

RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;

RA Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,

RA Byrne C.D., Fong K.J., Meer K., Patthy L.;

RT "The recurring evolution of lipoprotein(a). Insights from cloning of

RT hedgehog apolipoprotein(a).";

RL J. Biol. Chem. 270:24004-24009(1995).

RN [2]

RN SEQUENCE REVISION.

RA Lawn R.M.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor. Its role in tissue remodeling and tumor invasion may be modulated by CSPG4.

-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

-!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.

-!- SUBUNIT: Interacts with CSPG4 (By similarity).

-!- SUBCELLULAR LOCATION: Secreted protein.

-!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By similarity).

-!- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-582, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).

-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

-!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.

-!- SIMILARITY: Contains 5 kringle domains.

-!- SIMILARITY: Contains 1 PAN domain.

-!- SIMILARITY: Contains 1 peptidase S1 domain.

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EMBL; U33171; AAC48717.1; -; mRNA.

PIR; I46260; I46260.

HSSP; P00747; 1BUI.

SMR; Q29485; 568-810.

MEROPS; S01.233; -.

InterPro; IPR000001; Kringle.

InterPro; IPR003014; PAN.

InterPro; IPR003609; Pan\_app.

InterPro; IPR011358; Pept\_S1A\_plasmin.

InterPro; IPR001254; Peptidase\_S1\_S6.

InterPro; IPR001314; Peptidase\_S1A.

InterPro; IPR003966; Peptidase\_S1A\_pp.

Pfam; PF00051; Kringle; 5.

Pfam; PF00024; PAN\_1; 1.

Pfam; PF00089; Trypsin; 1.

PIRSF; PIRSF001150; Plasmin; 1.

PRINTS; PRO0722; CHYMOTRYPSIN.

PRINTS; PRO0018; KRINGLE.

PRINTS; PRO1505; PROTHROMBIN.

ProDom; PD000395; Kringle; 5.

SMART; SM00130; KR; 5.

SMART; SM00473; PAN\_AP; 1.

SMART; SM00020; TRYPSIN; 1.

PROSITE; PS00021; KRINGLE\_1; 5.

PROSITE; PS00070; KRINGLE\_2; 5.

PROSITE; PS00948; PAN; 1.

PROSITE; PS0240; TRYPSIN\_DOM; 1.

PROSITE; PS00134; TRYPSIN\_HIS; 1.

PROSITE; PS00135; TRYPSIN\_SER; 1.

KW Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;

KW Protease; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.

SIGNAL 1 19 By similarity.

CHAIN 20 810 Plasminogen.

/FTID=PRO\_0000028046.

FT CHAIN 20 582 Plasmin heavy chain A (By similarity).

/FTID=PRO\_0000028047.

FT PEPTIDE 20 97 Activation peptide (By similarity).

/FTID=PRO\_0000028048.





RES: 15  
 PLMN MACEU  
 ID PLMN MACEU STANDARD; PRT; 806 AA.  
 AC 018783;  
 DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JAN-1998, sequence version 1.  
 DT 07-MAR-2006, entry version 40.  
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;  
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light  
 DE chain B].  
 GN Name=PLG;  
 OS Macropus eugenii (Tamar wallaby).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
 OX NCBI\_TaxID=9315;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RC TISSUE=Liver;  
 RX MEDLINE=98004511; PubMed=9342350; DOI=10.1073/pnas.94.22.11992;  
 RA Lawn R.M., Schwartz K., Patchy L.;  
 RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).  
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenases and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von  
 CC Willebrand factor. Its role in tissue remodeling and tumor  
 CC invasion may be modulated by CSPG4 (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen  
 CC activators, both plasminogen and its activator being bound to  
 CC fibrin. Activated with catalytic amounts of streptokinase (By  
 CC similarity).  
 CC -!- SUBUNIT: Interacts with CSPG4 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted protein.  
 CC -!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By  
 CC similarity).  
 CC -!- PTM: In the presence of the inhibitor, the activation involves  
 CC only cleavage after Arg-576, yielding two chains held together by  
 CC two disulfide bonds. In the absence of the inhibitor, the  
 CC activation involves additionally the removal of the activation  
 CC peptide (By similarity).  
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin  
 CC immediately after dissociation from the clot (By similarity).  
 CC -!- MISCELLANEOUS: In the presence of the inhibitor, the activation  
 CC involves only cleavage after Arg-576, resulting in 2 chains held  
 CC together by 2 disulfide bonds. Without the inhibitor, the  
 CC activation involves also removal of the activation peptide (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 5 kringle domains.  
 CC -!- SIMILARITY: Contains 1 PAN domain.  
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF012297; AAB65760.1; -; mRNA.  
 DR HSSP; P00747; 1BUT.  
 DR SMR; O18783; 561-806.  
 DR MEROPS; S01.233; -.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR InterPro; IPR011358; Pept S1A\_Plasmin.  
 DR InterPro; IPR001254; Peptidase\_S1\_S6.  
 DR InterPro; IPR001314; Peptidase\_S1A.

DR InterPro; IPR003966; Peptidase\_S1A\_pp.  
 DR Pfam; PF00051; Kringle; 5.  
 DR Pfam; PF00024; PAN\_1; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR FIRSF; FIRSF001150; Plasmin; 1.  
 DR PRINTS; PRO0722; CHYMOTRYPSIN.  
 DR PRINTS; PRO0018; KRINGLE.  
 DR PRINTS; PRO1505; PROTHROMBIN.  
 DR ProDom; PD000395; Kringle; 5.  
 DR SMART; SM00130; KR; 5.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 5.  
 DR PROSITE; PS00070; KRINGLE\_2; 5.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Blood coagulation; Fibrinolysis; Hydrolase; Kringle; Repeat;  
 KW Serine protease; Signal; Tissue remodeling; Zymogen.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 806 Plasminogen.  
 FT /FTID=PRO\_0000028064.  
 FT CHAIN 20 576 Plasmin heavy chain A (By similarity).  
 FT /FTID=PRO\_0000028065.  
 FT PEPTIDE 20 96 Activation peptide (By similarity).  
 FT /FTID=PRO\_0000028066.  
 FT CHAIN 97 576 Plasmin heavy chain A, short form (By  
 FT similarity).  
 FT /FTID=PRO\_0000028067.  
 FT CHAIN 577 806 plasmin light chain B (By similarity).  
 FT /FTID=PRO\_0000028068.  
 FT DOMAIN 20 98 PAN.  
 FT DOMAIN 102 181 Kringle 1.  
 FT DOMAIN 184 262 Kringle 2.  
 FT DOMAIN 274 352 Kringle 3.  
 FT DOMAIN 370 448 Kringle 4.  
 FT DOMAIN 475 555 Kringle 5.  
 FT DOMAIN 577 804 Peptidase S1.  
 FT ACT\_SITE 618 Charge relay system (By similarity).  
 FT ACT\_SITE 661 Charge relay system (By similarity).  
 FT ACT\_SITE 756 Charge relay system (By similarity).  
 FT DISULFID 49 73 By similarity.  
 FT DISULFID 53 61 By similarity.  
 FT DISULFID 103 181 By similarity.  
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 FT DISULFID 152 176 By similarity.  
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 FT DISULFID 476 555 By similarity.  
 FT DISULFID 497 538 By similarity.  
 FT DISULFID 526 550 By similarity.  
 FT DISULFID 563 681 Interchain (between A and B chains) (By  
 FT similarity).  
 FT DISULFID 573 581 Interchain (between A and B chains) (By  
 FT similarity).  
 FT DISULFID 603 619 By similarity.  
 FT DISULFID 695 762 By similarity.  
 FT DISULFID 725 741 By similarity.  
 FT DISULFID 752 780 By similarity.  
 FT DISULFID 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;  
 SQ SEQUENCE

Query Match 75.3%; Score 1160; DB 1; Length 806;  
 Best Local Similarity 71.7%; Pred. No. 2.5e-80;  
 Matches 185; Conservative 34; Mismatches 39; Indels 0; Gaps 0;





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GenCore version 5.1.9  
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2006, 13:56:28 ; Search time 39 Seconds  
(without alignments)  
641.445 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSEKTKGKNGYRTWSK.....TNSQVRWEYCKIPDCSSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- PIR 80:\*
- 1: PIR1:\*
  - 2: PIR2:\*
  - 3: PIR3:\*
  - 4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1535	99.7	810	1 PLHU	plasmin (EC 3.4.21)
2	1442	93.6	810	2 B30848	plasmin (EC 3.4.21)
3	1292	83.9	790	1 PLPG	plasmin (EC 3.4.21)
4	1291	83.8	812	1 PLBO	plasmin (EC 3.4.21)
5	1274	82.7	812	1 PLMS	plasmin (EC 3.4.21)
6	1237	80.3	810	2 I46260	plasmin (EC 3.4.21)
7	891	57.2	2869	2 T18518	apolipoprotein(a)
8	797	51.8	728	1 JH0579	hepatocyte growth
9	782	50.8	728	1 A35644	hepatocyte growth
10	776.5	50.4	720	1 I51283	hepatocyte growth
11	776	50.4	718	1 A60185	hepatocyte growth
12	766.5	49.8	716	1 JCS061	macrophage-stimula
13	754.5	49.0	411	2 I51285	hepatocyte growth
14	753.5	48.9	716	1 A40332	macrophage-stimula
15	749	48.6	4548	1 S00657	apoptrotein(a) (EC
16	739	48.0	711	1 A47136	macrophage-stimula
17	739	48.0	1420	2 A32869	apolipoprotein(a)
18	505	32.8	455	2 A61545	plasmin (EC 3.4.21)
19	499	32.4	460	2 B61545	plasmin (EC 3.4.21)
20	391.5	25.4	336	2 S33879	plasmin precursor
21	372	24.2	625	1 TBBO	thrombin (EC 3.4.2
22	362.5	23.5	169	2 A40522	plasmin (EC 3.4.21
23	357.5	23.2	618	2 A35827	thrombin (EC 3.4.2
24	351	22.8	622	1 TBHU	thrombin (EC 3.4.2
25	348	22.6	617	2 S10511	thrombin (EC 3.4.2
26	309.5	20.1	562	1 UKHUT	t-plasminogen acti
27	265.5	19.2	559	1 A35029	t-plasminogen acti
28	281.5	18.3	559	1 A29941	t-plasminogen acti
29	278	18.1	120	2 E61545	plasmin (EC 3.4.21

30	271	17.6	89	2 A60140	plasmin (EC 3.4.21
31	268	17.4	123	2 C61545	plasmin (EC 3.4.21
32	241.5	15.7	937	2 A45082	neurotrophic recep
33	240	15.6	943	2 B45082	neurotrophic recep
34	237.5	15.4	946	1 A47299	ror-related recept
35	233	15.1	603	2 S28941	coagulation factor
36	214	13.9	558	2 JC5878	plasma hyaluronan-
37	210	13.6	560	1 JC4795	plasma hyaluronan-
38	201	13.1	291	2 I38098	t-plasminogen acti
39	198	12.9	615	1 KFHU12	coagulation factor
40	190.5	12.4	593	2 S45281	coagulation factor
41	188.5	12.2	655	1 A46688	hepatocyte growth
42	178.5	11.6	806	2 T18840	hypothetical prote
43	165	10.7	433	1 JN0560	u-plasminogen acti
44	153	9.9	442	1 UKPG	u-plasminogen acti
45	151	9.8	432	1 S18932	u-plasminogen acti

ALIGNMENTS

plasmin (EC 3.4.21.7) precursor [validated] - human

N:Alternate names: plasminogen precursor [misnomer]

N:Contains: angiotensin; microplasmin; plasminogen

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004

C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A046

R:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.

J. Biol. Chem. 265, 6104-6111, 1990

A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrin

A:Reference number: A35229; MUID:90202879; PMID:2318848

A:Accession: A35229

A:Molecule type: DNA

A:Residues: 1-810 <PEP>

A:Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UMI2; UNIPARC:UPI0000016AEC

A:Experimental source: leukocyte; lung fibroblast

R:Malgarutti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tar

Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990

A:Title: Definition of the transcription initiation site of human plasminogen gene in li

A:Reference number: I52242; MUID:91097523; PMID:2268308

A:Accession: I52242

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <MAL1>

A:Cross-references: UNIPARC:UPI00000062A8; GB:M62890; NID:G190092; PIDN:AAA36454.1; PID:G

R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.

FEBS Lett. 213, 254-260, 1987

A:Title: Molecular cloning and characterization of a full-length cDNA clone for human pla

A:Reference number: A26646; MUID:87162490; PMID:3030813

A:Accession: A26646

A:Molecule type: mRNA

A:Residues: 1-471, 'D', 473-810 <FOR>

A:Cross-references: UNIPARC:UPI00000008B8; GB:X05199; NID:G35530; PIDN:CRA28831.1; PID:G

A:Experimental source: liver

R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and t

A:Reference number: I45961; MUID:85023311; PMID:6148961

A:Accession: I62738

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 292-471, 'D', 473-810 <MAL2>

A:Cross-references: UNIPARC:UPI000016AED4; GB:K02922; NID:G190112; PIDN:AAA60124.1; PID:G

A:Accession: I84609

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 367-419 <MAL3>

A:Cross-references: UNIPARC:UPI0000071C7D; GB:K02921; NID:G190110; PIDN:AAA60123.1; PID:G

R:Brinsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;

Eur. J. Biochem. 114, 465-470, 1981

A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, t

A:Reference number: S03735; MUID:81212097; PMID:7238497  
 A:Accession: S03735  
 A:Molecule type: protein  
 A:Residues: 20-71, 'E', 73-76 <BRU>  
 A:Cross-references: UNIPARC:UPI0000172B8C  
 R:Sottrup-Jensen, L.; Petersen, T.E.; Magnusson, S.  
 submitted to the Atlas, July 1977  
 A:Reference number: A00929  
 A:Accession: A00929  
 A:Molecule type: protein  
 A:Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>  
 A:Cross-references: UNIPARC:UPI0000172B8D  
 R:Wiman, B.  
 Eur. J. Biochem. 76, 129-137, 1977  
 A:Title: Primary structure of the B-chain of human plasmin.  
 A:Reference number: A04627; MUID:7725245; PMID:142009  
 A:Accession: A04627  
 A:Molecule type: protein  
 A:Residues: 581-810 <W11>  
 A:Cross-references: UNIPARC:UPI00001450B9  
 R:Wiman, B.; Wallen, P.  
 Eur. J. Biochem. 50, 489-494, 1975  
 A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen  
 A:Reference number: A04625; MUID:75093329; PMID:122932  
 A:Accession: A04625  
 A:Molecule type: protein  
 A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>  
 A:Cross-references: UNIPARC:UPI0000172B8E  
 R:Wiman, B.; Wallen, P.  
 Eur. J. Biochem. 58, 539-547, 1975  
 A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen  
 A:Reference number: A04626; MUID:76043692; PMID:126863  
 A:Accession: A04626  
 A:Molecule type: protein  
 A:Residues: 483-507, 'E', 509-604 <W13>  
 A:Cross-references: UNIPARC:UPI0000172B8F  
 R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.  
 J. Biol. Chem. 248, 1631-1633, 1973  
 A:Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen  
 A:Reference number: A92125; MUID:73149248; PMID:4694729  
 A:Contents: annotation; active site  
 R:Groskopf, W.R.; Summaria, L.; Robbins, K.C.  
 J. Biol. Chem. 244, 3590-3597, 1969  
 A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a  
 A:Reference number: A92048; MUID:69234739; PMID:4240117  
 A:Contents: annotation; active site  
 R:Trexler, M.; Vali, Z.; Patthy, L.  
 J. Biol. Chem. 257, 7401-7406, 1982  
 A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.  
 A:Reference number: A92382; MUID:82213905; PMID:6919539  
 A:Contents: annotation; omega-aminocarboxylic acid binding sites  
 R:Vali, Z.; Patthy, L.  
 J. Biol. Chem. 259, 13690-13694, 1984  
 A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential  
 A:Reference number: A92458; MUID:85054794; PMID:6094526  
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site  
 R:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;  
 J. Biol. Chem. 271, 29461-29467, 1996  
 A:Title: Kringle domains of human angiotensin. Characterization of the anti-proliferative  
 A:Reference number: A58811; MUID:97067211; PMID:8910613  
 A:Contents: annotation  
 R:Uijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.  
 Biochemistry 37, 4699-4702, 1998  
 A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M  
 A:Reference number: A58812; MUID:9548733; PMID:9548733  
 A:Contents: annotation  
 R:Tulinsky, A.; Mulichak, A.M.  
 submitted to the Brookhaven Protein Data Bank, July 1991  
 A:Reference number: A51341; PDB:1PK4  
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454  
 R:Tulinsky, A.; Wu, T.P.  
 submitted to the Brookhaven Protein Data Bank, July 1991

A:Reference number: A51488; PDB:2PK4  
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454  
 R:Wu, T.P.; Tulinsky, A.  
 submitted to the Brookhaven Protein Data Bank, August 1993  
 A:Reference number: A51911; PDB:1PKR  
 A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181  
 R:Padmanabhan, K.; Tulinsky, A.  
 submitted to the Brookhaven Protein Data Bank, April 1994  
 A:Reference number: A52408; PDB:1PMK  
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454  
 R:Tulinsky, A.; Mathews, I.I.  
 submitted to the Brookhaven Protein Data Bank, December 1995  
 A:Reference number: A65244; PDB:1CEA  
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
 R:Tulinsky, A.; Mathews, I.I.  
 submitted to the Brookhaven Protein Data Bank, December 1995  
 A:Reference number: A65245; PDB:1CEB  
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
 R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.  
 Biochemistry 30, 10576-10588, 1991  
 A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å  
 A:Reference number: A58819; MUID:92031502; PMID:1657148  
 A:Contents: annotation  
 R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.  
 Biochemistry 30, 10589-10594, 1991  
 A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin  
 A:Reference number: A58818; MUID:92031503; PMID:1657149  
 A:Contents: annotation  
 R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.I.  
 Biochemistry 31, 270-279, 1992  
 A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4  
 A:Reference number: A39483; MUID:92118803; PMID:1310033  
 A:Contents: annotation; X-ray crystallography, 2.4 angstroms  
 R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.  
 submitted to the Brookhaven Protein Data Bank, June 1995  
 A:Reference number: A65980; PDB:1KRN  
 A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454  
 R:Rejante, M.; Llinas, M.  
 submitted to the Brookhaven Protein Data Bank, August 1996  
 A:Reference number: A58803; PDB:1HPJ  
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181  
 R:Rejante, M.; Llinas, M.  
 submitted to the Brookhaven Protein Data Bank, August 1996  
 A:Reference number: A65804; PDB:1HPK  
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181  
 R:Rejante, M.R.; Llinas, M.  
 Eur. J. Biochem. 221, 927-937, 1994  
 A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.  
 A:Reference number: S43645; MUID:94237157; PMID:8181475  
 A:Contents: annotation; conformation by (1)H-NMR, residues 96-184  
 R:Rejante, M.R.; Llinas, M.  
 Eur. J. Biochem. 221, 939-949, 1994  
 A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen  
 A:Reference number: A58817; MUID:94237158; PMID:8181476  
 A:Contents: annotation; conformation by (1)H-NMR  
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many other  
 C:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU at  
 C:PIR:KGUGB).  
 C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately after  
 rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,  
 C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial condi  
 C:Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. To  
 ting solid tumors.  
 C:Genetics:  
 A:Gene: GDB:PLG  
 A:Cross-references: GDB:119498; OMIM:173350  
 A:Map position: 6q26-q27  
 A:Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529/  
 C:Function:  
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a var  
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen acti  
 C:Pathway: fibrinolysis  
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;

C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolase; plasminogen-related protein precursor homology <PLPH>  
 F;1-19/Domains: signal sequence #status predicted <SIG>  
 F;20-810/Product: plasminogen #status experimental <PRO>  
 F;20-96/Domains: activation peptide #status experimental <APT>  
 F;79-466/Product: angiotensin #status experimental <AST>  
 F;97-580.581-810/Product: plasmin #status experimental <MAT>  
 F;97-580/Domains: plasmin chain A #status experimental <CHA>  
 F;103-181/Domains: kringle homology <KR1>

Query Match 99.7%; Score 1535; DB 1; Length 810;  
 Best Local Similarity 99.6%; Pred. No. 1.6e-104;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRTGKTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60  
 DB 98 VYLSECKTGNGKNYRTGKTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPHAH 120  
 DB 158 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPHAH 217

QY 121 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 180  
 DB 218 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 277

QY 181 GTGNYRGNAVTVSGHTCQHSQAQTPHTHPENFPCKNLDENYCRNPDGKRAPWCHT 240  
 DB 278 GTGNYRGNAVTVSGHTCQHSQAQTPHTHPENFPCKNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 2  
 B30848  
 Plasmin (EC 3.4.21.7) precursor - rhesus macaque  
 C;Species: Macaca mulatta (rhesus macaque)  
 C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C;Accession: B32869; B30848  
 R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.  
 J. Biol. Chem. 264, 5957-5965, 1989  
 A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.  
 A;Reference number: A32869; MUID:89174660; PMID:2925643  
 A;Accession: B32869  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-810 <TOM>  
 A;Cross-references: UNIPROT:P12545; UNIPARC:UPI0000131COP; CB:J04697; NID:G342272; PIDN:  
 C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
 F;1-9/Domains: plasminogen-related protein precursor homology <PLPH>  
 F;1-9/Domains: signal sequence #status predicted <SIG>  
 F;103-181/Domains: kringle homology <KR1>  
 F;185-262/Domains: kringle homology <KR2>  
 F;275-352/Domains: kringle homology <KR3>  
 F;377-454/Domains: kringle homology <KR4>  
 F;481-560/Domains: kringle homology <KR5>  
 F;581-803/Domains: trypsin homology <TRY>  
 F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32  
 bonds: #status predicted  
 F;622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2; Length 810;  
 Best Local Similarity 93.1%; Pred. No. 9.4e-98;  
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRTGKTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60  
 DB 98 VYLSECKTGNGKNYRTGKTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPHAH 120

DB 158 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPHAH 217

QY 121 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 180  
 DB 218 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 277

QY 181 GTGNYRGNAVTVSGHTCQHSQAQTPHTHPENFPCKNLDENYCRNPDGKRAPWCHT 240  
 DB 278 GTGNYRGNAVTVSGHTCQHSQAQTPHTHPENFPCKNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 3  
 PLPG  
 plasmin (EC 3.4.21.7) precursor - pig (fragment)  
 N;Alternate names: plasminogen  
 N;Contains: miniplasminogen  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 07-Sep-1990 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C;Accession: S03733; S03737; A25834  
 R;Schaller, J.; Marti, T.; Roesseler, S.J.; Kaempfer, U.; Rickli, E.E.  
 Fibrinolysis 1, 91-102, 1987  
 A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the car  
 A;Reference number: S03733  
 A;Accession: S03733  
 A;Molecule type: protein  
 A;Residues: 1-560 <SCH>  
 A;Cross-references: UNIPROT:P06867; UNIPARC:UPI0000172B90  
 R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;  
 Eur. J. Biochem. 114, 465-470, 1981  
 A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, i  
 A;Reference number: S03735; MUID:81212097; PMID:7238497  
 A;Accession: S03737  
 A;Molecule type: protein  
 A;Residues: 1-57 <BRU>  
 A;Cross-references: UNIPARC:UPI0000172B91  
 R;Marti, T.; Schaller, J.; Rickli, E.E.  
 Eur. J. Biochem. 149, 279-285, 1985  
 A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.  
 A;Reference number: A25834; MUID:85203907; PMID:3846533  
 A;Accession: A25834  
 A;Molecule type: protein  
 A;Residues: 450-790 <MAR>  
 A;Cross-references: UNIPARC:UPI0000172B92  
 C;Function:  
 A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vai  
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen acti  
 C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;  
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine protei  
 F;1-790/Product: plasminogen #status predicted <PRO>  
 F;1-77/Domains: plasminogen-related protein precursor homology (fragment) <PLPH>  
 F;1-77/Domains: activation peptide #status predicted <APT>  
 F;78-560/Product: plasmin chain A #status predicted <ACH>  
 F;84-162/Domains: kringle homology <KR1>  
 F;166-243/Domains: kringle homology <KR2>  
 F;256-333/Domains: kringle homology <KR3>  
 F;358-435/Domains: kringle homology <KR4>  
 F;450-790/Product: miniplasminogen #status experimental <MIN>  
 F;461-540/Domains: kringle homology <KR5>  
 F;561-790/Product: plasmin chain B #status experimental <BCH>  
 F;561-783/Domains: trypsin homology <TRY>  
 F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-  
 bonds: #status predicted  
 F;602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1; Length 790;  
 Best Local Similarity 81.4%; Pred. No. 8e-87;  
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

```
QY 1 VYLSECKTGNGKNYRGTMKNGITCKQWSSTSPHRPRFSPATHPSRGLSENYCRNPDN 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 IYVLECKTGNGKNYRGTMKNGITCKQWSSTSPHRPRFSPATHPSRGLSENYCRNPDN 138
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DPOGPWCYTTDPEKRYDYCDILECEECMHCSGENYDGKISKTMGLSCQAWDSQSPHAH 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 DEKGPCWYTTDPEKRYDYCDILECEECMHCSGENYDGKISKTMGLSCQAWDSQSPHAH 198
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GYIPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 199 GYLPSKFPNKNLKNYCRNPDGEPKPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 258
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHRTHTPENFPCKNLDENYCRNPDGKRAPWCHT 240
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 259 GRGENYRGTVSVTAGHTCQRWSAQSPHKHNRTPENFPCKNLDENYCRNPDGKRAPWCHT 318
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 TNSQVRWEYCKIPSCDSS 258
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 319 TDSEVRWDYCKIPSCSS 336
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 4
PLMO
Plasmin (EC 3.4.21.7) precursor - bovine
N:Alternate names: plasminogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text_change 09-Jul-2004
C:Accession: S45046; A25835; I45961; S03736
R:Berghlund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A:Description: Cloning and characterization of the bovine plasminogen cDNA.
A:Reference number: S45046
A:Accession: S45046
A:Molecule type: mRNA
A:Residues: 1-812 <BER>
A:Cross-references: UNIPROT:P06868; UNIPARC:UPI0000043BBB; EMBL:X79402; NID:G494962; PID:
A:Experimental source: liver
R:Note: It is uncertain whether Met-1 or Met-8 is the initiator
R:Schaller, J.; Moser, P.W.; Danneberg-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
Eur. J. Biochem. 149, 267-278, 1985
A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plas
A:Reference number: A25835; MUID:85203906; PMID:3846532
A:Accession: A25835
A:Molecule type: protein
A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
A:Cross-references: UNIPARC:UPI0000172B95
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A:Reference number: I45961; MUID:85023311; PMID:6148961
A:Accession: I45961
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 706-743, 'R', 745-812 <MAL>
A:Cross-references: UNIPARC:UPI000016C365; GB:K02935; NID:G163551; PIDN:AAA30714.1; PID:
R:Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Mameberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
A:Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03736
A:Molecule type: protein
A:Residues: 27-83 <BRU>
A:Cross-references: UNIPARC:UPI0000172B96
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
F1-26/Domain: signal sequence #status predicted <SIG>
F18-103/Domain: plasminogen-related protein precursor homology <PLPH>
F127-812/Product: plasminogen #status experimental <PRO>
```

```
F127-103/Domain: activation peptide #status experimental <APT>
F104-583,584-812/Product: plasmin #status experimental <MAT>
F104-583/Domain: plasmin chain A #status experimental <ACH>
F110-188/Domain: kringle homology <KR1>
F192-269/Domain: kringle homology <KR2>
F1282-359/Domain: kringle homology <KR3>
F1384-461/Domain: kringle homology <KR4>
F1485-564/Domain: kringle homology <KR5>
F1584-812/Domain: plasmin chain B #status experimental <BCH>
F1584-805/Domain: trypsin homology <TRY>
F156-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,333
bonds: #status predicted
F1315/Binding site: carbohydrate (Asn) (covalent) #status experimental
F1365/Binding site: carbohydrate (Ser) (covalent) #status experimental
F1624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 83.8%; Score 1291; DB 1; Length 812;
Best Local Similarity 80.8%; Pred. NO. 9.8e-87;
Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMKNGITCKQWSSTSPHRPRFSPATHPSRGLSENYCRNPDN 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 105 IYVLECKTGNGQTRGTGTTAETKSGVTCOKWSATSPKPFSPKPLAGLENYCRNPDN 164

QY 61 DPOGPWCYTTDPEKRYDYCDILECEECMHCSGENYDGKISKTMGLSCQAWDSQSPHAH 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 165 DENGPCWYTTDPEKRYDYCDILECEECMHCSGENYDGKISKTMGLSCQAWDSQSPHAH 224

QY 121 GYIPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 225 GYIPSKFPNKNLKNYCRNPDGEPKPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 284

QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHRTHTPENFPCKNLDENYCRNPDGKRAPWCHT 240
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 285 GTGKNYGTVAVTSGHTCQRWSAQSPHKHNRTPENFPCKNLDENYCRNPDGKRAPWCHT 344

QY 241 TNSQVRWEYCKIPSCDSSPV 260
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 345 TNSEVRWEYCTIPSCSSPL 364

RESULT 5
PLMS
Plasmin (EC 3.4.21.7) precursor - mouse
N:Contains: angiotatin; plasminogen
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: A38514; S48202; S48203
R:Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A:Title: Characterization of the cDNA coding for mouse plasminogen and localization of ti
A:Reference number: A38514; MUID:91184812; PMID:2081600
A:Accession: A38514
A:Molecule type: mRNA
A:Residues: 1-812 <DEG>
A:Cross-references: UNIPROT:P20918; UNIPARC:UPI0000028B2; GB:J04766; NID:G200402; PIDN:
R:Luijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A:Title: Characterization of the murine plasma fibrinolytic system.
A:Reference number: S48202; MUID:95010076; PMID:7523120
A:Accession: S48202
A:Molecule type: protein
A:Residues: 20-25 <LIJ>
A:Cross-references: UNIPARC:UPI0000172B93
A:Accession: S48203
A:Molecule type: protein
A:Residues: 22-27 <LI2>
A:Cross-references: UNIPARC:UPI0000172B93
C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth
C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmic
mediately after dissociation from the clot. In the presence of the inhibitor, the activat
e inhibitor, the activation involves also removal of the activation peptide.
C:Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiotatin. To
```

eful in treating solid tumors.

C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of tissues; also activates the urokinase-type plasminogen activator

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:19-19/Domain: signal sequence #status predicted <SIG>

F:20-812/Product: plasminogen #status predicted <PRO>

F:20-96/Domain: activation peptide #status predicted <APT>

F:79-466/Product: angiotensin #status predicted <AST>

F:97-581.582-812/Product: plasmin #status predicted <MAT>

F:97-581/Domain: chain A #status predicted <ACH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:582-812/Domain: chain B #status predicted <BCH>

F:582-805/Domain: trypsin homology <TRY>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,342-352/Domain: #status predicted

F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F:136-308/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted

F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental

F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 82.7%; Score 1274; DB 1; Length 812;

Best Local Similarity 80.6%; Pred. No. 1.7e-85;

Matches 208; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDN 60

DB 98 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDN 157

QY 61 DQGPWCYTTDEPKRYDYCDILECEBECMHCSGENTGDKISKTMSGLCQAWDSQSPHAA 120

DB 158 DQGPWCYTTDEPKRYDYCDILECEBECMHCSGENTGDKISKTMSGLCQAWDSQSPHAA 217

QY 121 GYIPSKFPNNKLNKNCYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTTQCLK 180

DB 218 GYIPSKFPNNKLNKNCYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTTQCLK 277

QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCCKNLDENYCRNPDGKRAPWCHT 240

DB 278 GRGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCCKNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSS 258

DB 338 TDSQVRWEYCKIPSCDSS 355

RESULT 6

I46260

Plasmin (EC 3.4.21.7) precursor - western European hedgehog

C:Species: Erinaceus europaeus (western European hedgehog)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004

C:Accession: I46260

R:Lawn, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein

A:Reference number: 146259; MUID:96025778; PMID:7592597

A:Accession: I46260

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-810 <LAW>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: hydrolase; serine proteinase

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:379-456/Domain: kringle homology <KR4>

F:482-561/Domain: kringle homology <KR5>

F:582-803/Domain: trypsin homology <TRY>

Query Match 80.3%; Score 1237; DB 2; Length 810;

Best Local Similarity 77.9%; Pred. No. 8.4e-83;

Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDN 60

DB 98 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDN 157

QY 61 DQGPWCYTTDEPKRYDYCDILECEBECMHCSGENTGDKISKTMSGLCQAWDSQSPHAA 120

DB 158 DQGPWCYTTDEPKRYDYCDILECEBECMHCSGENTGDKISKTMSGLCQAWDSQSPHAA 217

QY 121 GYIPSKFPNNKLNKNCYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTTQCLK 180

DB 218 GYIPSKFPNNKLNKNCYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTTQCLK 277

QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCCKNLDENYCRNPDGKRAPWCHT 240

DB 278 GRGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCCKNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSS 258

DB 338 TNSQVRWEYCKIPSCDSS 355

RESULT 7

T18518

apolipoprotein(a) - western European hedgehog (fragment)

C:Species: Erinaceus europaeus (western European hedgehog)

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T18518

R:Lawn, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein

A:Reference number: 146259; MUID:96025778; PMID:7592597

A:Accession: T18518

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2869 <LAW>

A:Cross-references: UNIPROT:Q28398; UNIPARC:UPI000008785C; EMBL:U33170; NID:g1046358; PII

A:Experimental source: liver

C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, consists of

ent apolipoprotein(a).

Query Match 57.2%; Score 881; DB 2; Length 2869;

Best Local Similarity 55.0%; Pred. No. 2.7e-56;

Matches 149; Conservative 36; Mismatches 70; Indels 16; Gaps 3;

QY 3 LSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDNDP 62

DB 2495 VDQCLEGTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDNDP 2553

QY 63 QGPWCYTTDEPKRYDYCDILECEBECMHCSGENTGDKISKTMSGLCQAWDSQSPHAA 110

DB 2554 VAPWCYTTDEPKRYDYCDILECEBECMHCSGENTGDKISKTMSGLCQAWDSQSPHAA 2613

QY 111 AWDSQSPHAAHGYIPSKFPNNKLNKNCYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPP 170

DB 2614 GWRKQTPHREYTPENYPSKLNFGNVCYCRNPDGELAPWCYTTNSAVRWEYCSIPTCSSSP 2673

QY 171 SSGPTY---QCLKGTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDNDP 227

DB 2674 PTEPMIIPDQCLEGTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRFSPATHPSGLSENYCRNPDNDP 2733

QY 228 RNPDKGRAPWCHTNSQVRWEYCKIPSCDSS 258

DB 2734 RNPDKGRAPWCHTNSQVRWEYCKIPSCDSS 2764

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RESULT 8
JH0579
hepatocyte growth factor precursor [validated] - human
N:Alternate names: hepatolentin A; scatter factor
C:Species: Homo sapiens (man)
C>Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text change 09-Jul-2004
C:Accession: JH0579; J03333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796; S06
R:Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A:Title: Organization of the human hepatocyte growth factor-encoding gene.
A:Reference number: JH0579; MUID:91340155; PMID:1831432
A:Accession: JH0579
A:Molecule type: DNA
A:Residues: 1-728 <SEK>
A:Cross-references: UNIPROT:P14210; UNIPARC:UPI000000D92B; DBJ:D90318
A>Note: the authors translated the codon GAA for residue 662 as Gly
R:Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A:Description: Organization of the human hepatocyte growth factor-encoding gene.
A:Reference number: JH0579
A:Accession: JH0579
A:Molecule type: DNA
A:Residues: 1-481,'RT',484-728 <SE2>
A:Cross-references: UNIPARC:UPI0000172B97
R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandeckerkhove, J.; Weingart, S.; Rieder, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth f
A:Reference number: A41140; MUID:91334393; PMID:1831266
A:Accession: A41140
A:Molecule type: mRNA
A:Residues: 1-728 <WEI>
A:Cross-references: UNIPARC:UPI000000D92B; GB:M73239; NID:g337935; PIDN:AAAS4239.1; PID:
R:Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth facto
A:Reference number: A36677; MUID:91025062; PMID:2145836
A:Accession: B36677
A:Molecule type: mRNA
A:Residues: 1-728 <SE3>
A:Cross-references: UNIPARC:UPI000000D92B; GB:M60718; NID:g184031; PIDN:AAAS2648.1; PID:
A:Accession: A36677
A:Molecule type: mRNA
A:Residues: 1-161,167-728 <SE4>
A:Cross-references: UNIPARC:UPI0000146316; EMBL:X16323
R:Experimental source: leukocyte
R:Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
A:Reference number: A33512; MUID:89392017; PMID:2528952
A:Accession: A33512
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-728 <MIY>
A:Cross-references: UNIPARC:UPI000000D92B; GB:M29145; NID:g184041; PIDN:AAAS2650.1; PID:
R:Rubin, J.S.; Chan, A.M.L.; Botcaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
A:Reference number: A39006; MUID:91110540; PMID:1824873
A:Accession: A39006
A:Molecule type: mRNA
A:Residues: 1-161,167-728 <RUB>
A:Cross-references: UNIPARC:UPI0000146316; GB:M55379
R:Experimental source: embryonic lung
R:Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A:Title: Identification of the N-terminal residue of the heavy chain of both native and
A:Reference number: PH0114; MUID:91207365; PMID:1826837
A:Accession: PH0114
A:Molecule type: protein
A:Residues: 32-43;53-58 <YOS>
A:Cross-references: UNIPARC:UPI0000172B98; UNIPARC:UPI0000172B99

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A:Experimental source: plasma
R:Weidner, K.M.; Behrens, J.; Vandeckerkhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990
A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of epit
A:Reference number: A37796; MUID:91035621; PMID:2146276
A:Accession: A37796
A:Molecule type: protein
A:Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',54
A:Cross-references: UNIPARC:UPI0000172B9A; UNIPARC:UPI0000172B9B; UNIPARC:UPI0000172B9C;
R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashii
Nature 342, 440-443, 1989
A:Title: Molecular cloning and expression of human hepatocyte growth factor.
A:Reference number: S06794; MUID:90066676; PMID:2531289
A:Accession: S06794
A:Molecule type: mRNA
A:Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'W',301-316,'A',318-335,'K',337-386,'N'
A:Cross-references: UNIPARC:UPI000015624E; EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:
R:Experimental source: liver
A>Note: the authors translated the codon CAG for residue 727 as Glu
A:Note: part of this sequence, including the amino end of both the alpha and beta chains,
R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchme
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth facto
A:Reference number: I59214; MUID:93087571; PMID:1280830
A:Accession: I59214
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-288,'ET',<HAR>
A:Cross-references: UNIPARC:UPI0000073BF9; GB:L02931; NID:g184033; PIDN:AAAS2649.1; PID:
R:Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor ge
A:Reference number: S15443; MUID:91200041; PMID:1826653
A:Accession: S15443
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-288,'ET',<MIY2>
A:Cross-references: UNIPARC:UPI0000073BF9; EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:
R:Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
A:Reference number: I52253; MUID:92062058; PMID:1835383
A:Accession: I52253
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 161-166 <SHI>
A:Cross-references: UNIPARC:UPI00000353AB; GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:
C:Genetics:
A:Gene: GDB:HGF
A:Cross-references: GDB:127524; OMIM:142409
A:Map position: 7q21.1-7q21.1
A:Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 481
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Function:
A:Description: stimulates mitosis of hepatocytes and other cells
A:Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringlike homolog
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringlike; pyro
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>
F:32-494/Domain: alpha chain #status experimental <ACH>
F:128-206/Domain: kringlike homology <KR1>
F:211-288/Domain: kringlike homology <KR2>
F:305-383/Domain: kringlike homology <KR3>
F:391-469/Domain: kringlike homology <KR4>
F:495-728/Domain: beta chain #status experimental <BCH>
F:495-716/Domain: trypsin homology <TRY>
F:32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F:294,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:487-604/Disulfide bonds: #status predicted
Query Match 51.8%; Score 797; DB 1; Length 728;
Best Local Similarity 51.0%; Pred. No. 9.4e-51;

```



Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;

QY 2 YLSECKTGNGKNGYRGTMTSKNGITCQKWSSTSPHRRPSPATHPSGLEENYCRNPND 61  
 DB 124 YIRNCIIIGRSGYKGTSTKSGIKQCPWNSMIPHEHSFLPSSYRGKDLQENYCRNPRGE 183  
 QY 62 POGPWCYTTDPKRYDYCDILECEE-ECMHCSGENTYDGKISKTMSGLECOAWDSQSPHAH 120  
 DB 184 EGGPWCFTSNPEVRVEVCDIPQCSVECTCNGESYRGLMDHTESKICQWDHQTPHRH 243  
 QY 121 GYIPSKFPNKLKKNYCRNPDRRLRPWCFTTDPNKEWELCDIPRC--TTPPSSGP--TY 176  
 DB 244 KFLPERYPDKGDDNYCRNPDRGPRWCYTLDPHTRWECYCAIKCADNTMNDTDPLETT 303  
 QY 177 QCLKGTGENTYRGNVAVTSGHTCOHWSAQTPHTERTPENFPCKNLDENYCRNPDKRAP 236  
 DB 304 ECIQGGEGYRGVTNTIWIINGIPQCRWDSQYPHEDMTPEFCKOLRENYCRNPDSSEP 363  
 QY 237 WCHTTSQVRWEYC-KIPSCDSS 258  
 DB 364 WCFTTDPNIRVGYCSQIPNCDMS 386

RESULT 9  
 A35644  
 hepatocyte growth factor precursor - rat  
 N/Alternate names: hepatolentin A; scatter factor  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 28-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 09-Jul-2004  
 C/Accession: A35644; S13211  
 R/Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamura, Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990  
 A/Title: Deduced primary structure of rat hepatocyte growth factor and expression of the A/Reference number: A35644; MUID:90222197; PMID:2139229  
 A/Accession: A35644  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-728 <TAS>  
 A/Cross-references: UNIPROT:P17945; UNIPARC:UPI000012C6D3; GB:D90102; GB:M32987; NID:922 R/Okajima, A.; Miyazawa, K.; Kitamura, N. Eur. J. Biochem. 193, 375-381, 1990  
 A/Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur A/Reference number: S13211; MUID:91031482; PMID:2146117  
 A/Accession: S13211  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-728 <OKA>  
 A/Cross-references: UNIPARC:UPI000012C6D3; EMBL:X54400; NID:956353; PIDN:CAA38266.1; PID C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
 C/Function:  
 A/Description: stimulates mitosis of hepatocytes and other cells  
 A/Note: does not have proteinase activity  
 C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog F/1-32/Domain: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr F/56-495/Product: signal sequence #status predicted <SIG>  
 F/56-495/Product: hepatocyte growth factor #status predicted <MAT>  
 F/129-207/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
 F/212-289/Domain: kringle homology <KR1>  
 F/306-384/Domain: kringle homology <KR2>  
 F/392-470/Domain: kringle homology <KR3>  
 F/496-719/Domain: kringle homology <KR4>  
 F/496-719/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
 F/33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F/295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted F/488-607/Disulfide bonds: #status predicted  
 Query Match 50.8%; Score 782; DB 1; Length 728;  
 Best Local Similarity 49.8%; Pred. No. 1.2e-49;  
 Matches 132; Conservative 39; Mismatches 84; Indels 10; Gaps 4;

QY 2 YLSECKTGNGKNGYRGTMTSKNGITCQKWSSTSPHRRPSPATHPSGLEENYCRNPND 61

DB 125 YIRNCIIIGRSGYKGTSTKSGIKQCPWNSMIPHEHSFLPSSYRGKDLQENYCRNPRGE 184  
 QY 62 POGPWCYTTDPKRYDYCDILECEE-ECMHCSGENTYDGKISKTMSGLECOAWDSQSPHAH 120  
 DB 185 EGGPWCFTSNPEVRVEVCDIPQCSVECTCNGESYRGLMDHTESKICQWDHQTPHRH 244  
 QY 121 GYIPSKFPNKLKKNYCRNPDRRLRPWCFTTDPNKEWELCDIPRC--TTPPSSGP 174  
 DB 245 KFLPERYPDKGDDNYCRNPDRGPRWCYTLDPHTRWECYCAIKCADNTMNDTDPLETT 303  
 QY 175 QCLKGTGENTYRGNVAVTSGHTCOHWSAQTPHTERTPENFPCKNLDENYCRNPDKGR 234  
 DB 303 TTECIKGGEGYRGVTNTIWIINGIPQCRWDSQYPHEDMTPEFCKOLRENYCRNPDSSEP 362  
 QY 235 APWCHTTSQVRWEYC-KIPSCDSS 258  
 DB 363 SPWCFTTDPNIRVGYCSQIPNCDMS 387

RESULT 10  
 I51283  
 hepatocyte growth factor precursor - clawed frog  
 N/Alternate names: hepatolentin A; scatter factor  
 C/Species: Xenopus sp. (clawed frog)  
 C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-May-2004  
 C/Accession: I51283  
 R/Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiohawa, K. Mech. Dev. 49, 123-131, 1995  
 A/Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus earl A/Reference number: I51283; MUID:95267690; PMID:7748783  
 A/Accession: I51283  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-710 <NAK>  
 A/Cross-references: UNIPARC:UPI00000FDFB6; GB:S77422; NID:9998932; PIDN:AAB34354.1; PID:9 A/Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleotic C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
 C/Function:  
 A/Description: stimulates mitosis of hepatocytes and other cells  
 A/Note: does not have proteinase activity  
 C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog C/Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle F/42-477/709/Product: hepatocyte growth factor #status predicted <MAT>  
 F/42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
 F/115-193/Domain: kringle homology <KR1>  
 F/198-275/Domain: kringle homology <KR2>  
 F/289-367/Domain: kringle homology <KR3>  
 F/375-453/Domain: kringle homology <KR4>  
 F/478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
 F/478-709/Domain: trypsin homology <TRY>  
 F/52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pred F/470-588/Disulfide bonds: #status predicted  
 Query Match 50.4%; Score 776.5; DB 1; Length 710;  
 Best Local Similarity 50.0%; Pred. No. 2.9e-49;  
 Matches 130; Conservative 39; Mismatches 88; Indels 3; Gaps 3;

QY 2 YLSECKTGNGKNGYRGTMTSKNGITCQKWSSTSPHRRPSPATHPSGLEENYCRNPND 61  
 DB 111 YIRDCIHGKSGNYRGTNTKGLACQCPWNSMIPHEHSFLPSTYRGKDLKKNYCRNPKGE 170  
 QY 62 POGPWCYTTDPKRYDYCDILECEE-ECMHCSGENTYDGKISKTMSGLECOAWDSQSPHAH 120  
 DB 171 EGGPWCFTSNPEVRVEVCDIPFCEVDCVTCNGEYRGPMDYTESGKECQWDLPQPHKH 230  
 QY 121 GYIPSKFPNKLKKNYCRNPDRRLRPWCFTTDPNKEWELCDIPRC--TTPPSSGP 179  
 DB 231 KFLPERYPNKLNDNYCRNPDKGRPWCYTLDPHTRWECYCAIKCADNTMNDTDPLETT 290  
 QY 180 KGTGENTYRGNVAVTSGHTCOHWSAQTPHTERTPENFPCKNLDENYCRNPDKGRAPWCH 239  
 DB 291 KQGGEGYRGSVSTTYNGIQCRWDSQYPHEDMTPEFCKOLSENYCRNPDSSEP 350



F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>  
F:489-709/Domain: trypsin homology <TRY>  
F:72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.0%; Score 754.5; DB 1; Length 411;  
Best Local Similarity 50.2%; Pred. No. 6.7e-48;  
Matches 132; Conservative 31; Mismatches 89; Indels 11; Gaps 4;

QY 2 YLSECKTGNKGNVGTMSKTNGITCKQWSSSPHPRSPATHPSEGLEENYCRNPND 61  
DB 106 YVRTCIMDNGSVRGTVARTAGLPCQWSSRPFPNDHKYTF--PKNGLEENCRNPDDG 163  
QY 62 PQGPWCYTTDPKRYDYCDILECEE--CMHCSENYDGKISKTMSGLEQWDSQSPHAH 120  
DB 164 PRGPWCYTTNRSVRPQSGIKTCREAVCVLCNGEDYRGEVDVTESGRCQWDLQPHSH 223  
QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRC--TTPPSSGTYQ- 177  
DB 224 PPHPEKFPDKALKNDYCRNPDSASRPWCYTTDPNVEREFCDLPSCGPNLPPTTKGSKSQ 283  
QY 178 -----CLKGTGENYRGNVAVTSGHTCOHWSAQTPHTHTERTPENFPCKNLIDENYCRN 229  
DB 284 RNKVKASNCFRGKGYRGTWNTTSAGVPCQWDAQNPQHFRVPPEKYACKDLRENFERN 343  
QY 230 PDGKRAPWCHTNSQVRWEYC-KIPSCDSSPV 260  
DB 344 PDGSEAPWCFTRSPGLRVAFCQIPRCTEYV 375

RESULT 13  
I51285  
hepatocyte growth factor/scatter factor - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I51285  
R:Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard  
Developement 121, 813-824, 1995  
A:Title: A role for HGF/SP in neural induction and its expression in Hensen's node durin  
A:Reference number: I51285; MUID:95237013; PMID:7720585  
A:Accession: I51285  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-411 <STR>  
A:Cross-references: UNIPROT:Q90978; UNIPARC:UPI0000175C78; GB:S77480; NID:9998675; PID:9  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringie homolo  
F:124-197/Domain: kringie homology <KR3>  
F:202-279/Domain: kringie homology <KR2>  
F:296-374/Domain: kringie homology <KR3>

Query Match 49.0%; Score 754.5; DB 2; Length 411;  
Best Local Similarity 50.2%; Pred. No. 6.7e-48;  
Matches 132; Conservative 31; Mismatches 89; Indels 11; Gaps 4;

QY 2 YLSECKTGNKGNVGTMSKTNGITCKQWSSSPHPRSPATHPSEGLEENYCRNPND 61  
DB 120 YVNCILIGAGYKGTISITKSGIQQWNSMIPHE-----HSYKQDLRENYCRNPGE 174  
QY 62 PQGPWCYTTDPKRYDYCDILECEE--CMHCSENYDGKISKTMSGLEQWDSQSPHAH 120  
DB 175 EGGPWCFTTSPQWHEVCDIPLCSEVECTMGESYRGPMDHTESKEQWDLQPHKH 234  
QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRC--TTPPSSGTYQ- 176  
DB 235 KFRPERYPDKGDDNYCRNPDKGLRWCYTTDPNTEWFECAIKTCDVGLNSTEVAETT 294  
QY 177 QCLKGTGENYRGNVAVTSGHTCOHWSAQTPHTHTERTPENFPCKNLIDENYCRNPDKRAP 236  
DB 295 TCIQGGEGYRGTWNTTSAGVPCQWDSQFPQHNTITPENFPCKNLIDENYCRNPDSGSE 354  
QY 237 WCHTNSQVRWEYC-KIPSCDSS 258  
DB 355 WCFTTDPNIRIGCSQIPKCDVS 377

## RESULT 14

A40332

macrophage-stimulating protein 1 precursor - mouse  
N:Alternate names: hepatocyte growth factor-like protein  
C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: A40332; B40332

R:Degeen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.  
Biochemistry 30, 9781-9791, 1991

A:Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor

A:Reference number: A40332; MUID:92002017; PMID:1832957

A:Accession: A40332

A:Molecule type: DNA

A:Residues: 1-716 <DEG>

A:Cross-references: UNIPROT:P26928; UNIPARC:UPI000000402B; GB:M74180; NID:g193831; PID:N

A:Molecule type: mRNA

A:Residues: 1-18, 'p', 20-716 <DEG2>

A:Cross-references: UNIPARC:UPI0000027E40; GB:M74181; NID:g193833; PIDN:AAAS0167.1; PID:5

C:Genetics:

A:Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 470

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor

C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringie homolo

C:Keywords: duplication; glycoprotein; growth factor; kringie

F:1-31/Domain: signal sequence #status predicted <SIG>

F:19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>

F:19-483/Domain: alpha chain #status experimental <ACH>

F:110-186/Domain: kringie homology <KR1>

F:191-268/Domain: kringie homology <KR2>

F:292-370/Domain: kringie homology <KR3>

F:379-457/Domain: kringie homology <KR4>

F:484-711/Domain: beta chain #status experimental <BCH>

F:489-709/Domain: trypsin homology <TRY>

F:72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.9%; Score 753.5; DB 1; Length 716;

Best Local Similarity 48.3%; Pred. No. 1.4e-47;

Matches 129; Conservative 37; Mismatches 86; Indels 15; Gaps 5;

QY 2 YLSECKTGNKGNVGTMSKTNGITCKQWSSSPHPRSPATHPSEGLEENYCRNPND 61

DB 106 YVRTCIMDNGSVRGTVARTAGLPCQWSSRPFPNDHKYTF--PKNGLEENCRNPDDG 163

QY 62 PQGPWCYTTDPKRYDYCDILECEE--CMHCSENYDGKISKTMSGLEQWDSQSPHAH 120

DB 164 PRGPWCYTTNRSVRPQSGIKTCREAVCVLCNGEDYRGEVDVTESGRCQWDLQPHSH 223

QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRC--TTPPP----- 170

DB 224 PFQPEKFLDKLDKNDYCRNPDSGSRPWCYTTDPNVEREFCDLPSCGPNLPPTVKGSKSQ 283

QY 171 -SSGPTYQCLKGTGENYRGNVAVTSGHTCOHWSAQTPHTHTERTPENFPCKNLIDENYCRN 229

DB 284 RNKRALNCFRGKGYRGTWNTTSAGVPCQWDAQNPQHFRVPPEKYACKDLRENFERN 343

QY 230 PDGKRAPWCHTNSQVRWEYC-KIPSC 255

DB 344 PDGSEAPWCFTRSPGLRVAFCQIPRC 370

## RESULT 15

S00657

apoptote(a) (BC 3.4.21.-) precursor [validated] - human

N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286

R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scan

Nature 330, 132-137, 1987

A:Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.

A:Reference number: S00657; MUID:88039109; PMID:3670400

A:Accession: S00657

F	1396-1473/Domain:	kringle homology <KR13>	
F	1510-1587/Domain:	kringle homology <KR14>	
F	1624-1701/Domain:	kringle homology <KR15>	
F	1738-1815/Domain:	kringle homology <KR16>	
F	1852-1929/Domain:	kringle homology <KR17>	
F	1966-2043/Domain:	kringle homology <KR18>	
F	2080-2157/Domain:	kringle homology <KR19>	
F	2194-2271/Domain:	kringle homology <KR20>	
F	2308-2385/Domain:	kringle homology <KR21>	
F	2422-2499/Domain:	kringle homology <KR22>	
F	2536-2613/Domain:	kringle homology <KR23>	
F	2650-2727/Domain:	kringle homology <KR24>	
F	2764-2841/Domain:	kringle homology <KR25>	
F	2878-2955/Domain:	kringle homology <KR26>	
F	2992-3069/Domain:	kringle homology <KR27>	
F	3106-3183/Domain:	kringle homology <KR28>	
F	3220-3297/Domain:	kringle homology <KR29>	
F	3334-3411/Domain:	kringle homology <KR30>	
F	3448-3525/Domain:	kringle homology <KR31>	
F	3562-3639/Domain:	kringle homology <KR32>	
F	3676-3753/Domain:	kringle homology <KR33>	
F	3782-3859/Domain:	kringle homology <KR34>	
F	3896-3973/Domain:	kringle homology <KR35>	
F	4010-4087/Domain:	kringle homology <KR36>	
F	4124-4201/Domain:	kringle homology <KR37>	
F	4228-4307/Domain:	kringle homology <KR38>	
F	4328-4541/Domain:	trypsin homology <TRY>	
Query Match 48.6%; Score 749; DB 1; Length 4548;			
Best Local Similarity 41.2%; Pred. No. 1.8e-46;			
Matches 129; Conservative 45; Mismatches 81; Indels 58; Gaps 5;			
Qy	3	LSECKTNGKNYRGTWKTKNGITCQKWSSTSPHRPRFSPATHPSGLENYCRNPNDP	62
Db	3779	VQDCYHGDSQSRGSPSTTVTGRTCQSSWMTPHWHQRTTEYYPNGGLTRNYCRNPDAEI	3838
Qy	63	QGWCYCTDPEKVDYCDILEE-----EEDM	89
Db	3839	R-PWCYITDPSVRWEYCNLTQCPVMSSTLLTTVTVPVPSTELPSEAPTENSTGVQDCY	3897
Qy	90	HCSENYDGIKISMTSGLEQWDSQPHAGYIPSKFPNKNLKQNYCRNPDRRLRPWCF	149
Db	3898	RGDQSYRGTLSTITIGRTCQSSWTPHWHRIPLYYPNAGLTRNYCRNPDAEIRPCWY	3957
Qy	150	TTDPNKGWEJCDIPRC-----TTP-----PPSGGPTVQ-CLKGTGEN	185
Db	3958	TMDPSVRWEYCNLTFCPVTSESSVLTPTTVPAPVPSTEAPSEQAPPEKSPVVQDCYHGDSR	4017
Qy	186	YRGNAVTVSGHTCQWSAOTPHTHERTPENFFCKNLDENYCRNPDKRAPWCHTINSQV	245
Db	4018	YRGLSSTTVTGRTCQSSWMIPIHWHQRTPENYPNAGLTRNYCRNPDSGKQPCWYCTDPCV	4077
Qy	246	RWEYCKIPSCDSS	258
Db	4078	RWYECNLTQCSSET	4090

Search completed: August 29, 2006, 14:01:59  
Job time : 40 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model  
Run on: August 29, 2006, 13:51:34 ; Search time 199 Seconds  
(without alignments)  
597.368 Million cell updates/sec

Title: US-09-502-176-2  
Perfect score: 1540  
Sequence: 1 VYLSEKTEGKNGYRTGMSK.....TNSQVRWEYCKIPCDSSPV 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A Geneseq 8:\*
- 1: geneseqp1980s:\*
  - 2: geneseqp1990s:\*
  - 3: geneseqp2000s:\*
  - 4: geneseqp2001s:\*
  - 5: geneseqp2002s:\*
  - 6: geneseqp2003as:\*
  - 7: geneseqp2003bs:\*
  - 8: geneseqp2004s:\*
  - 9: geneseqp2005s:\*
  - 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1540	100.0	260	3	AAB26486	Aab26486 Deglycosy
2	1540	100.0	260	4	AAU01209	Aau01209 Human Ang
3	1537	99.8	869	7	ADK40316	Adk40316 C-termina
4	1537	99.8	869	7	ADK40314	Adk40314 N-termina
5	1535	99.7	260	6	AAQ79748	Aaq79748 Human pla
6	1535	99.7	268	2	AAQ72109	Aaq72109 A multifu
7	1535	99.7	285	2	AAQ72102	Aaq72102 A multifu
8	1535	99.7	339	2	AAQ83961	Aaq83961 Human pla
9	1535	99.7	339	2	AAW07581	Aaw07581 N-Termina
10	1535	99.7	339	2	AAW94038	Aaw94038 Human ang
11	1535	99.7	339	4	AAW50318	Aaw50318 Human ang
12	1535	99.7	339	7	ADG47024	Adg47024 Human ang
13	1535	99.7	339	8	ADM11543	Adm11543 Human pla
14	1535	99.7	339	9	AED08938	Aed08938 Human ang
15	1535	99.7	339	9	AED64669	Aed64669 Human ang
16	1535	99.7	363	3	AAV70255	Aav70255 Human ang
17	1535	99.7	364	2	AAV702106	Aav702106 A multifu
18	1535	99.7	374	3	AAV79226	Aav79226 Angiogene
19	1535	99.7	375	3	AAV79225	Aav79225 Angiogene
20	1535	99.7	378	2	AAW07579	Aaw07579 Human kri
21	1535	99.7	378	3	AAW16450	Aaw16450 Human ang
22	1535	99.7	378	5	AAW48894	Aaw48894 Human ang
23	1535	99.7	378	7	ADG47063	Adg47063 Human kri

24	1535	99.7	378	9	AED08977	Aed08977 Human kri
25	1535	99.7	380	2	AAV02105	Aav02105 A multifu
26	1535	99.7	381	2	AAV02101	Aav02101 A multifu
27	1535	99.7	391	6	ADA08454	Ada08454 Mammalian
28	1535	99.7	391	8	ADP67426	Adp67426 A61 anti-
29	1535	99.7	394	6	ADA08455	Ada08455 Mammalian
30	1535	99.7	394	8	ADP67427	Adp67427 A61 anti-
31	1535	99.7	452	3	AAV79224	Aav79224 Angiogene
32	1535	99.7	453	2	AAV02093	Aav02093 A multifu
33	1535	99.7	453	2	AAV02099	Aav02099 A multifu
34	1535	99.7	453	2	AAV02095	Aav02095 A multifu
35	1535	99.7	453	2	AAV02096	Aav02096 A multifu
36	1535	99.7	453	2	AAW95051	Aaw95051 Amino aci
37	1535	99.7	470	2	AAV02112	Aav02112 A multifu
38	1535	99.7	480	7	ABU64288	Abu64288 Human ang
39	1535	99.7	484	6	AAG79749	Aag79749 Human pla
40	1535	99.7	563	5	ABB75942	Abb75942 Endotheli
41	1535	99.7	566	2	AAV02100	Aav02100 A multifu
42	1535	99.7	571	5	ABB75944	Abb75944 Angiotens
43	1535	99.7	576	5	ABB75943	Abb75943 Angiotens
44	1535	99.7	579	8	ADG82532	Adg82532 Prolactin
45	1535	99.7	654	8	ABM83810	Abm83810 Human dia

ALIGNMENTS

RESULT 1  
AAB26486  
ID AAB26486 standard; protein; 260 AA.  
AC AAB26486;  
XX  
DT 16-JAN-2001 (first entry)  
XX  
DE Deglycosylated kringle 1-5 region protein.  
XX  
KW Deglycosylated; kringle; angiogenesis; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200047729-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 10-FEB-2000; 2000WO-US003482.  
XX  
PR 10-FEB-1999; 99US-0119562P.  
XX  
PR 07-APR-1999; 99US-0128062P.  
XX  
PA (ENTR-) ENTREMED INC.  
PA (CHIL-) CHILDRENS MEDICAL CENT.  
XX  
PI Pirie-Shepherd S, Folkman MJ, Liang H, Macdonald NJ, Sim KL;  
XX  
DR WPI; 2000-579032/54.  
XX  
N-ESDB; AAA94906.  
XX  
PT Novel composition comprising deglycosylated fragments of kringle 1-5 regions of plasminogen linked to the glycosylated form, useful for inhibiting angiogenesis.  
XX  
XX Claim 7; Fig 1; 42pp; English.  
XX  
CC The present sequence is deglycosylated kringle 1-5 region protein.  
CC Deglycosylated kringle 1-5 region protein has increased antiangiogenic activity as compared to glycosylated kringle 1-5 region protein. The  
CC deglycosylated kringle 1-5 region protein was isolated from human  
XX plasminogen by affinity chromatography  
SQ Sequence 260 AA;  
Query Match 100.0%; Score 1540; DB 3; Length 260;

02 Local Similarity 100.0%; Pred. No. 1.1e-90; Mismatches 0; Indels 0; Gaps 0;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60  
QY 61 DPGSPWCYTTDPEKRYDYCDILECEECMHCSCGENYDGKISKTMGLGCQAWDSQSPH 120  
DB 61 DPGSPWCYTTDPEKRYDYCDILECEECMHCSCGENYDGKISKTMGLGCQAWDSQSPH 120  
QY 121 GYIPSKFPNKNLKNYCRNPDRELRCWCFPTDPRKRWELCDIPRCTTPPPSSGPTYOCLK 180  
DB 121 GYIPSKFPNKNLKNYCRNPDRELRCWCFPTDPRKRWELCDIPRCTTPPPSSGPTYOCLK 180  
QY 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 2  
AAU01209  
ID AAU01209 standard; protein; 260 AA.  
XX AC AAU01209;  
XX DT 26-SEP-2001 (first entry)  
XX DE Human Angiostatin (hASv3) protein.  
XX KW Human; Angiostatin; recombinant production; cation exchange column; fermentation; angiogenesis mediated disease; leukaemia; tumour;  
XX KW rheumatoid arthritis; plaque neovascularisation.  
XX OS Homo sapiens.  
XX FN WO200140260-A2.  
XX PD 07-JUN-2001.  
XX PP 04-DEC-2000; 2000WO-US032843.  
XX PR 03-DEC-1999; 99US-0168919P.  
XX PA (ENTR-) ENTREMED INC.  
XX PI Madsen J, Liang H, Sim KL, Zhou X, Chang-Murad A, Boerner RJ;  
XX PI Bermejo LL, Mistry FR, Schrimsher JL, Shepard SR;  
XX DR WPI; 2001-408277/43.  
XX DR N-PSDB; AAS04181.  
XX PT Purifying recombinant angiostatin, involves applying fermented broth containing angiostatin to expanded bed cation exchange column, and anion exchange column, hydroxyapatite column, hydrophobic column and a membrane.  
XX PS Example 1; Page 22; 49pp; English.  
XX CC The present sequence representing Angiostatin protein is given in an invention providing a method for recombinant production, recovery and purification of Angiostatin protein. Purification of recombinant Angiostatin comprises applying crude fermentation broth containing the protein to an expanded bed cation exchange column, eluting it, and applying the eluate to anion exchange column, repeating the process of eluting and applying, to hydroxyapatite column, hydrophobic column and membrane, in order, and collecting fluid passing through the membrane. Angiostatin is useful for treating angiogenesis mediated diseases, including solid tumours, leukaemia, tumour metastases, benign tumours,

CC rheumatoid arthritis, psoriasis, ocular angiogenic diseases, Osler-Webber syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiofibroma and wound granulation. CC As a centrifugation technique is not employed in the process, damage to the cells with concomitant release of undesirable biological materials such as cytochromes, pigments, enzymes, chemicals and other undesirable cellular constituents and debris, is prevented. Large scale recovery and purification of proteins is greater than that obtained from prior art methods. Active Angiostatin can be stored in buffers for extended periods of time, in vials or other containers, either in solution which may be liquid or frozen, or lyophilised  
XX SQ Sequence 260 AA;  
Query Match 100.0%; Score 1540; DB 4; Length 260;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90; Mismatches 0; Indels 0; Gaps 0; Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60  
QY 61 DPGSPWCYTTDPEKRYDYCDILECEECMHCSCGENYDGKISKTMGLGCQAWDSQSPH 120  
DB 61 DPGSPWCYTTDPEKRYDYCDILECEECMHCSCGENYDGKISKTMGLGCQAWDSQSPH 120  
QY 121 GYIPSKFPNKNLKNYCRNPDRELRCWCFPTDPRKRWELCDIPRCTTPPPSSGPTYOCLK 180  
DB 121 GYIPSKFPNKNLKNYCRNPDRELRCWCFPTDPRKRWELCDIPRCTTPPPSSGPTYOCLK 180  
QY 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 3  
ADK40316  
ID ADK40316 standard; protein; 869 AA.  
XX AC ADK40316;  
XX DT 06-MAY-2004 (first entry)  
XX DE C-terminal albumin-angiostatin fusion protein.  
XX KW Cytostatic; vaccine; albumin fusion protein;  
XX KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer; collagen.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO2003066085-A1.  
XX PD 14-AUG-2003.  
XX PF 07-FEB-2003; 2003WO-IB000433.  
XX PR 07-FEB-2002; 2002US-0355547P.  
XX PA (AVET) AVENTIS BEHRING GMBH.  
XX PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
XX PI Mertins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;  
XX WPI; 2003-731479/69.  
XX DR N-PSDB; ADK40315.  
XX PT New albumin fusion protein comprising an angiogenesis inhibiting peptide

PT and an albumin having an albumin activity, or their fragments or  
 PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.  
 XX  
 PS Disclosure; Fig 8; 136pp; English.  
 XX  
 CC The invention relates to an albumin fusion protein comprising an  
 CC angiogenesis inhibiting peptide and an albumin having an albumin  
 CC activity, or their fragments or variants. The albumin fusion proteins,  
 CC compositions, vaccines and methods are useful for treating angiogenesis-  
 CC dependent tumor, e.g. cancer. This sequence represents an C-terminal  
 CC albumin-angiostatin fusion protein.  
 XX  
 SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;  
 Best Local Similarity 99.8%; Pred. NO. 5.1e-90;  
 Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VYLSECKTGNGKNGYRTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
 DB 610 VYLSECKTGNGKNGYRTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 669  
 QY 61 DPOGWCYTTDPEKRYDYCDILECEBECMHCSGENTDGIKSTMSGLECOAWDSQSPFAH 120  
 DB 670 DPOGWCYTTDPEKRYDYCDILECEBECMHCSGENTDGIKSTMSGLECOAWDSQSPFAH 729  
 QY 121 GYIPSKFPNKLKKNYCRNPDRPDLRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTTQCLK 180  
 DB 730 GYIPSKFPNKLKKNYCRNPDRPDLRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTTQCLK 789  
 QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
 DB 790 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 849  
 QY 241 TNSQVREWEYCKIPSCDSSPV 260  
 DB 850 TNSQVREWEYCKIPSCDSSPV 869

RESULT 4  
 ADK40314  
 ID ADK40314 standard; protein; 869 AA.  
 XX  
 AC ADK40314;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE N-terminal angiostatin-albumin fusion protein.  
 XX  
 KW cytostatic; vaccine; albumin fusion protein;  
 KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;  
 KW collagen.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2003066085-A1.  
 XX  
 PD 14-AUG-2003.  
 XX  
 PF 07-FEB-2003; 2003WO-IB000433.  
 XX  
 PR 07-FEB-2002; 2002US-0355547P.  
 XX  
 PA (AVET ) AVENTIS BEHRING GMBH.  
 PA (DELZ ) DELTA BIOTECHNOLOGY LTD.  
 XX  
 PI Martins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;  
 XX  
 DR 2003-731479/69.  
 DR 1803; ADK40313.  
 XX  
 PT New albumin fusion protein comprising an angiogenesis inhibiting peptide  
 XX

PT and an albumin having an albumin activity, or their fragments or  
 PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.  
 XX  
 PS Disclosure; Fig 6; 136pp; English.  
 XX  
 CC The invention relates to an albumin fusion protein comprising an  
 CC angiogenesis inhibiting peptide and an albumin having an albumin  
 CC activity, or their fragments or variants. The albumin fusion proteins,  
 CC compositions, vaccines and methods are useful for treating angiogenesis-  
 CC dependent tumor, e.g. cancer. This sequence represents an N-terminal  
 CC angiostatin-albumin fusion protein.  
 XX  
 SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;  
 Best Local Similarity 99.8%; Pred. NO. 5.1e-90;  
 Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VYLSECKTGNGKNGYRTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
 DB 25 VYLSECKTGNGKNGYRTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 84  
 QY 61 DPOGWCYTTDPEKRYDYCDILECEBECMHCSGENTDGIKSTMSGLECOAWDSQSPFAH 120  
 DB 85 DPOGWCYTTDPEKRYDYCDILECEBECMHCSGENTDGIKSTMSGLECOAWDSQSPFAH 144  
 QY 121 GYIPSKFPNKLKKNYCRNPDRPDLRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTTQCLK 180  
 DB 145 GYIPSKFPNKLKKNYCRNPDRPDLRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTTQCLK 204  
 QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
 DB 205 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 264  
 QY 241 TNSQVREWEYCKIPSCDSSPV 260  
 DB 265 TNSQVREWEYCKIPSCDSSPV 284

RESULT 5  
 AAG79748  
 ID AAG79748 standard; protein; 260 AA.  
 XX  
 AC AAG79748;  
 XX  
 DT 18-MAR-2003 (first entry)  
 XX  
 DE Human plasminogen kringle domains 1-3, KL-3.  
 XX  
 KW Human; plasminogen; angiostatin; neovascularisation; kringle domain;  
 KW cell proliferation; viral vector; replication-defective; cancer; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200288173-A2.  
 XX  
 PD 07-NOV-2002.  
 XX  
 PF 29-APR-2002; 2002WO-US013461.  
 XX  
 PR 30-APR-2001; 2001US-0287673P.  
 PR 05-APR-2002; 2002US-0370634P.  
 XX  
 PA (CELL-) CELL GENESYS INC.  
 XX  
 PI Chang B, Wu WW, Macarthur J, Patel S, Jooss K, Mendez M;  
 XX  
 DR WPI; 2003-129131/12.  
 DR N-PSDB; ABA00776.  
 XX  
 PT New recombinant viral vector expressing human angiostatin useful for  
 PT inhibiting angiogenesis in a mammalian subject with cancer or tumor.  
 XX



PS closure; Page 75-76; 83pp; English.

XX This sequence represents kringle domains 1-3 of human plasminogen. A 38  
CC kD N-terminal fragment of plasminogen is referred to as angiotatin and  
CC inhibits neovascularisation. Angiotatin contains 4 kringle domains of  
CC the parent molecule. However, angiotatin containing all 4 kringle  
CC domains (K1-4) was found to be no more potent as an inhibitor of cell  
CC proliferation than an angiotatin only containing K1-3. Therefore,  
CC kringle 4 does not possess inhibitory activity. A fragment of the  
CC plasminogen coding sequence may be used in the recombinant viral vector  
CC of the invention for obtaining angiotatin activity. The vector comprises  
CC a promoter capable of expressing human angiotatin operably linked to a  
CC structural gene encoding one or more domains of human angiotatin. The  
CC vector, which may be a replication-defective viral vector, is useful for  
CC inhibiting angiogenesis in a mammal, especially with cancer or a tumour  
XX

SQ Sequence 260 AA;

Query Match 99.7%; Score 1535; DB 6; Length 260;  
Best Local Similarity 99.6%; Pred. No. 2.2e-90;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGMSKTNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGNYRTGMSKTNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCOQWDSQSPH 120  
DB 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCOQWDSQSPH 120  
QY 121 GYIPSKFPNNLKNKYNCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTQCLK 180  
DB 121 GYIPSKFPNNLKNKYNCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQPTHTNRTPEFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCOHWSAQPTHTNRTPEFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6  
AAY02109  
ID AAY02109 standard; protein; 268 AA.

XX AAY02109;

XX 16-JUL-1999 (first entry)

XX A multifunctional protein of the invention.

XX Angiotatin; endostatin; interferon; thrombospondin;  
KW interferon-inducible protein; platelet factor 4; anti-angiogenic;  
KW anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;  
KW diabetic retinopathy; macular degeneration; arthritis;  
KW tumor cell production.

XX Synthetic.

OS Homo sapiens.

XX WO9916889-A1.

XX 08-APR-1999.

XX 30-SEP-1998; 98WO-US020464.

XX 01-OCT-1997; 97US-0060609P.

XX (SEAR ) SEARLE & CO G D.

XX Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;

PI McKeam JP;

XX WPI; 1999-255098/21.

XX New multifunctional proteins useful for treating angiogenic-mediated diseases.

XX Claim 5; Page 104; 121pp; English.

XX The specification describes multifunctional proteins which comprise combinations of angiotatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the invention

XX Sequence 268 AA;

Query Match 99.7%; Score 1535; DB 2; Length 268;  
Best Local Similarity 99.6%; Pred. No. 2.3e-90;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGMSKTNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
DB 3 VYLSECKTGNGNYRTGMSKTNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 62  
QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCOQWDSQSPH 120  
DB 63 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCOQWDSQSPH 122  
QY 121 GYIPSKFPNNLKNKYNCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTQCLK 180  
DB 123 GYIPSKFPNNLKNKYNCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTQCLK 182  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQPTHTNRTPEFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 183 GTGENYRGNAVTVSGHTCOHWSAQPTHTNRTPEFPCKNLNDENYCRNPDGKRAPWCHT 242  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 243 TNSQVRWEYCKIPSCDSSPV 262

RESULT 7

AAY02102

ID AAY02102 standard; protein; 285 AA.

XX AAY02102;

XX 16-JUL-1999 (first entry)

XX A multifunctional protein of the invention.

XX Angiotatin; endostatin; interferon; thrombospondin;

KW interferon-inducible protein; platelet factor 4; anti-angiogenic;

KW anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;

KW diabetic retinopathy; macular degeneration; arthritis;

KW tumor cell production.

XX Synthetic.

OS Homo sapiens.

XX WO9916889-A1.

XX 08-APR-1999.



XX PF 30-SEP-1998; 98WO-US020464.  
 XX PD 01-OCT-1997; 97US-0060609P.  
 XX PR (SEAR ) SEARLE & CO G D.  
 XX PA Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;  
 PI McKearn JP;  
 XX WPI; 1999-255098/21.  
 XX New multifunctional proteins useful for treating angiogenic-mediated  
 PT diseases.  
 XX Claim 5; Page 97-98; 121pp; English.  
 XX The specification describes multifunctional proteins which comprise  
 CC combinations of angiotatin, endostatin, interferon, thrombospondin,  
 CC interferon-inducible protein and platelet factor 4, and have anti-  
 CC angiogenic and/or anti-tumor activity. The multifunctional protein may  
 CC exhibit useful properties such as having similar or greater biological  
 CC activity when compared to a single factor or by having improved half-life  
 CC or decreased adverse side effects, or a combination of these properties.  
 CC The proteins can be used for treating an angiogenic-mediated disease,  
 CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.  
 CC They can also be used for inhibiting the production of tumor cells  
 CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,  
 CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)  
 CC in a patient and for inhibiting tumor growth. The present sequence  
 CC represents a multifunctional protein of the invention  
 XX Sequence 285 AA;  
 SQ

Query Match 99.7%; Score 1535; DB 2; Length 285;  
 Best Local Similarity 99.6%; Pred. No. 2.4e-90;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
 DB 20 VYLSECKTGNGNYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 79  
 QY 61 DPQGPWCYTTPDKRYDYCDILECEECMHCSENYDGKISKTMGSLGCQAWDSQSPH 120  
 DB 80 DPQGPWCYTTPDKRYDYCDILECEECMHCSENYDGKISKTMGSLGCQAWDSQSPH 139  
 QY 121 GYIPSPKPNKLNKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180  
 DB 140 GYIPSPKPNKLNKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 199  
 QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 240  
 DB 200 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 259  
 QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 DB 260 TNSQVRWEYCKIPSCDSSPV 279

RESULT 8  
 AAR83961  
 ID AAR83961 standard; protein; 339 AA.  
 XX AC AAR83961;  
 XX DT 10-MAR-1996 (first entry)  
 XX 24-JUN-1997 (first entry)  
 XX N-Terminal angiotatin fragment.  
 XX angiotatin; plasminogen; endothelial inhibitor; therapeutic;  
 XX gene therapy.  
 OS Homo sapiens.

XX PN WO9529242-A1.  
 XX PD 02-NOV-1995.  
 XX PF 26-APR-1995; 95WO-US005107.  
 XX PR 26-APR-1994; 94US-00248629.  
 XX PR 20-OCT-1994; 94US-00328785.  
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX Oreilly MS, Folkman MJ, Sim KL, Cao Y;  
 XX WPI; 1995-382990/49.  
 XX Endothelial inhibitor Angiostatin - useful to treat angiogenic mediated  
 PT disease esp. angiogenesis and cancer.  
 XX Claim 4; Page 81-82; 108pp; English.  
 XX The sequence represents a plasminogen fragment which is compared with the  
 CC corresponding plasminogen fragments of monkey (AAR83962), pig (AAR83963)  
 CC and cattle (AAR83964) origin (in Fig.2), as well as the with the first  
 CC 339 amino acids of mouse angiotatin (AAR83960) (i.e. aa's 98-436 of the  
 CC complete 812 aa plasminogen molecule AAR83959). Human angiotatin is a  
 CC plasminogen fragment starting at aa 97 or 99 of the complete plasminogen  
 CC molecule. Angiotatin is an endothelial inhibitor, which reversibly  
 CC inhibits proliferation of endothelial cells and thereby inhibits  
 CC angiogenesis. It is useful in the treatment of a human or animal with  
 CC angiogenic mediated disease e.g. arthritis, macular degeneration,  
 CC diabetic retinopathy or cancer. Cells comprising angiotatin-coding  
 CC sequences are useful for gene therapy of primary tumors  
 XX Sequence 339 AA;  
 SQ

Query Match 99.7%; Score 1535; DB 2; Length 339;  
 Best Local Similarity 99.6%; Pred. No. 2.8e-90;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
 DB 1 VYLSECKTGNGNYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
 QY 61 DPQGPWCYTTPDKRYDYCDILECEECMHCSENYDGKISKTMGSLGCQAWDSQSPH 120  
 DB 61 DPQGPWCYTTPDKRYDYCDILECEECMHCSENYDGKISKTMGSLGCQAWDSQSPH 120  
 QY 121 GYIPSPKPNKLNKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180  
 DB 121 GYIPSPKPNKLNKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180  
 QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 240  
 DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 240  
 QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9  
 AAW07581  
 ID AAW07581 standard; protein; 339 AA.  
 XX AC AAW07581;  
 XX DT 24-JUN-1997 (first entry)  
 XX N-Terminal angiotatin fragment.  
 XX angiotatin; plasminogen; kringling; angiogenesis; cancer; arthritis;  
 XX macular degeneration; diabetic retinopathy.

XX 06-APR-1999 (first entry)  
XX Human angiotensin fragment.  
XX Plasminogen; kringle; endothelial; angiogenesis; tumour; leukaemia;  
XX rheumatoid arthritis; psoriasis; ocular angiogenic disease; ulcer;  
XX gene therapy; birth control; Crohn's disease; angiotensin.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX Peptide 6..255  
XX /note= "Kringle 1-3"  
XX Peptide 6..165  
XX /note= "Kringle 1-2"  
XX Peptide 6..84  
XX /note= "Kringle 1"  
XX Peptide 88..255  
XX /note= "Kringle 2-3"  
XX Peptide 88..165  
XX /note= "Kringle 2"  
XX Peptide 178..255  
XX /note= "Kringle 3"  
XX WO9854217-A1.  
XX 03-DEC-1998.  
XX 29-MAY-1998; 98WO-US010979.  
XX 30-MAY-1997; 97US-00866735.  
XX (CHIL-) CHILDRENS MEDICAL CENT.  
XX Folkman MJ, O'reilly MS;  
XX WPI; 1999-059809/05.  
XX Use of plasminogen fragments - having an amino acid sequence similar to  
XX the kringle 1-5 region, for inhibiting endothelial cell proliferation and  
XX angiogenesis.  
XX Example 27; Fig 2A-C; 165pp; English.  
XX The invention relates to inhibition of endothelial cell proliferation  
XX that comprises administering to an endothelial cell a plasminogen  
XX fragment having an amino acid sequence similar to the kringle 1-5 region  
XX of a plasminogen molecule. The plasminogen fragments can be derived from  
XX murine, human, Rhesus, porcine or bovine plasminogens. The plasminogen  
XX fragments can be used for modulating angiogenesis and treating angiogenic  
XX -mediated disease e.g. solid tumours; for treating excessive or abnormal  
XX stimulation of endothelial cells; as a birth control agent; and in the  
XX treatment of diseases that have angiogenesis as a pathological  
XX consequence (see AAW94036 for details on the various diseases the  
XX plasminogen fragments can be used to treat). The nucleotide sequences  
XX encoding the plasminogen fragments can also be used for gene therapy. The  
XX products can be used for the production of antibodies and in detection  
XX and diagnosis. Sequences AAW94037 to W4041 represent angiotensin  
XX fragments (protein derivatives of angiotensin or plasminogen, having an  
XX endothelial cell proliferation activity) of murine, human, Rhesus,  
XX porcine and bovine angiotensins respectively. The kringle regions that  
XX can be used in the invention are indicated in the features  
XX  
XX Sequence 339 AA;  
XX  
XX Query Match 99.7%; Score 1535; DB 2; Length 339;  
XX Best Local Similarity 99.6%; Pred. No. 2.8e-90;  
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60  
XX 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60  
XX 61 DPGPMCYTTDPKRYDYCDILECEBECMHCSGENTYDGKISKTMSGLEQAWDSQSPHAAH 120  
XX 61 DPGPMCYTTDPKRYDYCDILECEBECMHCSGENTYDGKISKTMSGLEQAWDSQSPHAAH 120  
XX 121 GYTPSPFNKLNKNCYRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPSSGPTVOCCLK 180  
XX 121 GYTPSPFNKLNKNCYRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPSSGPTVOCCLK 180  
XX 181 GTGENTRGVAVTVSGHTCQHWASQTPHTERTPEPNCNLDENYCRNPDGKRAPWCHT 240  
XX 181 GTGENTRGVAVTVSGHTCQHWASQTPHTERTPEPNCNLDENYCRNPDGKRAPWCHT 240  
XX 241 TNSQVRWEYCKIPSCDSSPV 260  
XX 241 TNSQVRWEYCKIPSCDSSPV 260  
XX  
XX RESULT 10  
XX AAW94038  
XX ID AAW94038 standard; protein; 339 AA.  
XX AC AAW94038;  
XX

XX 14-NOV-1996.  
XX WO9635774-A2.  
XX 26-APR-1996; 96WO-US005856.  
XX 26-APR-1995; 95US-00429743.  
XX 22-FEB-1996; 96US-00605598.  
XX 08-MAR-1996; 96US-00612788.  
XX (CHIL-) CHILDRENS MEDICAL CENT.  
XX Folkman MJ, Oreilly MS, Cao Y, Sim XL, Lin J;  
XX WPI; 1996-518662/51.  
XX Use of angiotensin fragments or aggregates - for inhibiting endothelial  
XX cell proliferation and treating angiogenesis-mediated diseases, e.g.  
XX cancer, arthritis or diabetic retinopathy.  
XX Claim 59; Page 96-97; 203pp; English.  
XX The invention relates to new methods and compositions for inhibiting  
XX endothelial cell proliferation, using as active component an angiotensin  
XX fragment, a combination of angiotensin fragments, or aggregate  
XX angiotensin. The fragment is preferably derived from murine, human,  
XX Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2,  
XX kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle  
XX 1-4BKLs protein. The aggregate angiotensin has a Mol. Wt. of 45-65 kD and  
XX is derived from a plasminogen fragment beginning at approximately amino  
XX acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen.  
XX The active component can be used for treating angiogenesis-mediated  
XX diseases such as cancer, arthritis, macular degeneration and diabetic  
XX retinopathy. It can also be used to develop antibodies for use in  
XX diagnosis, detection and therapy. The present sequence, which is the N-  
XX terminal fragment of human angiotensin, is a specific aggregate  
XX angiotensin which can be used in the invention  
XX  
XX Sequence 339 AA;  
XX  
XX Query Match 99.7%; Score 1535; DB 2; Length 339;  
XX Best Local Similarity 99.6%; Pred. No. 2.8e-90;  
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60  
XX 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60  
XX 61 DPGPMCYTTDPKRYDYCDILECEBECMHCSGENTYDGKISKTMSGLEQAWDSQSPHAAH 120  
XX 61 DPGPMCYTTDPKRYDYCDILECEBECMHCSGENTYDGKISKTMSGLEQAWDSQSPHAAH 120  
XX 121 GYTPSPFNKLNKNCYRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPSSGPTVOCCLK 180  
XX 121 GYTPSPFNKLNKNCYRNPDRRLPWCFTTDPNKEWELCDIPRCTTTPSSGPTVOCCLK 180  
XX 181 GTGENTRGVAVTVSGHTCQHWASQTPHTERTPEPNCNLDENYCRNPDGKRAPWCHT 240  
XX 181 GTGENTRGVAVTVSGHTCQHWASQTPHTERTPEPNCNLDENYCRNPDGKRAPWCHT 240  
XX 241 TNSQVRWEYCKIPSCDSSPV 260  
XX 241 TNSQVRWEYCKIPSCDSSPV 260  
XX  
XX RESULT 10  
XX AAW94038  
XX ID AAW94038 standard; protein; 339 AA.  
XX AC AAW94038;  
XX

QY 61 DPGWCYTTDPKRYDYCDILECEECMHCSGENYDGKISKTMSGLECOAWDSQSPHAH 120  
 DB 61 DPGWCYTTDPKRYDYCDILECEECMHCSGENYDGKISKTMSGLECOAWDSQSPHAH 120  
 QY 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180  
 DB 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180  
 QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 240  
 DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 240  
 QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 DB 241 TNSQVRWEYCKIPSCDSSPV 260

## RESULT 11

AAM50518  
 ID AAM50518 standard; protein; 339 AA.

XX AC AAM50518;

DT 12-MAR-2002 (first entry)

XX DE Human angiotatin.

XX KW Angiotatin; plasminogen; human; angiogenesis; endothelial cell;  
 KW cell proliferation; inhibitor; tumour; antipsoriatic; cytostatic;  
 KW vasotropic; antitumour; dermatological; antiinflammatory; antidiabetic;  
 KW antirheumatic; antiarthritic; ophthalmological; vulnery; antiulcer;  
 KW antibacterial; antiatherosclerotic; gynaecological; antipyretic;  
 KW cardiatic; contraceptive; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Region 6..255  
 FT /label= Kringle-1-3  
 FT Region 6..165  
 FT /label= Kringle-1-2  
 FT Region 6..84  
 FT /label= Kringle-1  
 FT Region 88..255  
 FT /label= Kringle-2-3  
 FT Region 88..165  
 FT /label= Kringle-2  
 FT Region 178..255  
 FT /label= Kringle-3

XX US2001029246-A1.

XX PN 11-OCT-2001.

XX PD 16-FEB-2001; 2001US-00788142.

XX PF 30-MAY-1997; 97US-00866735.

XX PR 24-APR-1998; 98US-00066028.

XX PR 11-MAY-1999; 99US-00303821.

XX PR 22-JUN-1999; 99US-00338387.

XX (OREI/) O'REILLY M S.

XX (FOLK/) FOLKMAN M J.

XX (CAOY/) CAO Y.

XX PI O'reilly MS, Folkman MJ, Cao Y;

XX DR 2001-647990/74.

XX PT Angiotatin endothelial cell proliferation, useful for treating angiogenic  
 PT mediated diseases such as cancer, arthritis, comprises administering  
 PT plasminogen fragment corresponding to kringle structures of plasminogen

PT molecule.

XX Example 27; Fig 2A-C; 70pp; English.

XX The present sequence is that of human angiotatin. A claimed method of  
 CC inhibiting endothelial cell proliferation involves administering a  
 CC plasminogen fragment (PF) having an amino acid sequence similar to the  
 CC kringle 1-5 region of a plasminogen molecule. This includes a protein,  
 CC termed angiotatin, defined by its ability to overcome the angiogenic  
 CC activity of endogenous growth factors and by its amino acid sequence  
 CC homology and structural similarity to an internal portion of plasminogen,  
 CC beginning at approximately amino acid 98. The PF is preferably derived  
 CC from mouse, human, Rhesus monkey, pig or cattle (see AAM50516-21). It is  
 CC used in methods and compositions for the treatment of an angiogenic-  
 CC mediated disease, including haemangioma, solid tumours, blood-borne  
 CC tumours, leukaemia, metastasis, telangiectasia, psoriasis,  
 CC atherosclerosis, scleroderma, pyogenic granuloma, myocardial  
 CC angiogenesis, Crohn's disease, plaque neovascularisation, coronary  
 CC collaterals, cerebral collaterals, arteriovenous malformations, ischaemic  
 CC limb angiogenesis, corneal diseases, rubeosis, neovascular glaucoma,  
 CC diabetic retinopathy, corneal graft rejection, retrolental fibroplasia,  
 CC haemophilic joints, rheumatoid arthritis, diabetic neovascularisation,  
 CC Osler-Webber syndrome, macular degeneration, wound healing, peptic ulcer,  
 CC Helicobacter pylori related diseases, fractures, keloids, vasculogenesis,  
 CC haematopoiesis, ovulation, menstruation, placentaion and cat scratch  
 CC fever. Angiotatin is also useful as a birth control agent by preventing  
 CC vascularisation required for embryo implantation. The compositions are  
 CC particularly useful for treating or repressing the growth of tumours.  
 CC Administration of angiotatin to a human or animal with prevascularised  
 CC metastasized tumours will prevent the growth or expansion of those  
 CC tumours. Gene therapy methods are also included in the invention

XX Sequence 339 AA;

Query Match 99.7%; Score 1535; DB 4; Length 339;

Best Local Similarity 99.6%; Pred. No. 2.8e-90;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60

DB 1 VYLSECKTGNGKNGRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60

QY 61 DPGWCYTTDPKRYDYCDILECEECMHCSGENYDGKISKTMSGLECOAWDSQSPHAH 120

DB 61 DPGWCYTTDPKRYDYCDILECEECMHCSGENYDGKISKTMSGLECOAWDSQSPHAH 120

QY 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180

DB 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180

QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 240

DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHRTPEPNCNLDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260

DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 12

ADG47024

ID ADG47024 standard; protein; 339 AA.

XX AC ADG47024;

XX DT 11-MAR-2004 (first entry)

XX DE Human angiotatin protein.

XX KW Angiotatin; cell proliferation; angiogenic-mediated disease; cancer;  
 KW arthritis; macular degeneration; diabetic retinopathy; psoriasis;  
 KW scleroderma; Crohn's disease; wounds; peptic ulcer; fracture;  
 KW gene therapy; plasminogen; cytostatic; ophthalmological; dermatological;

inflammatory; vulnery; human.

**Homoc sapiens.**

US2003064926-A1.

03-APR-2003.

22-APR-2002: 2002US-00127066.

26-APR-1994:

20-OCT-1994;  
26-APR-1995;

08-MAR-1996;  
30-MAY-1997:

24-APR-1998;  
11-MAY-1999;

17-JUN-1999;  
22-JUN-1999:

16-FEB-2001;

(FOLK/ ) FOLK/ )  
(O'REY/ ) O'REY/ )

(CAOY / ) CAO  
(CTMZ / ) CTM

8-11-66 NY

4  
L  
C  
C  
C  
4  
1

**SECRET**

arthritis or diabetic

fragment.

**Example 27; SEQ**

The present invention relates to endothelial

The invention is use

retinopathy, psoriasis, scleroderma, Crohn's disease, wounds, peptic ulcer and fractures. The invention is also useful in gene therapy. The present sequence is the human angiotensin protein.

Sequence 339 AA:

99.7%: Score 1535: DB 7: Length 339:

100% Local Similarity 99.6%; Pred. NO: 2.8e-50;  
 Mismatches 259: Conservative 0: Mismatches 1: Indels 0: Gaps

1 VYLSECKTNGKNGYRGTMSTKNGITCOKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 6

1 VVLSCKTGNCKNVPGTMSKTKNGITCOKWSSTSPHPRPRFSPATHPSEGLEENYCRNPDN 6

61 DPOGPWCYTTDPEKRYDVC DILECEEECMHCSENYDGKISKTMGLECOAWDSOSPAAH 1

61 DPOGPWCYTTDPEKRYDYCNLLCEEEECMHCSENYDGKISKTMGLECOAWDPSOPHAI 1

121 C Y T P S K F P N K N I . K K A Y C B N P D B E I . R P W C F T T P D N K R W E I . C F

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

101 STATEMENTS

[illegible]

## 013 MICROWAVE

[illegible]

LT 13



CC      ful in inhibiting vascular leakage, inflammation and fibrosis in an  
CC      animal having diabetes, chronic inflammation, brain edema, arthritis,  
CC      uveitis, macular edema, cancer, hyperglycemia, a kidney inflammatory  
CC      disease, a disorder resulting in kidney fibrosis and/or a disorder of the  
CC      kidney resulting in proteinuria. The present sequence is the human  
CC      angiotensin protein.  
XX  
SQ

Sequence 339 NA;

Query Match		99.7%;	Score 1535;	DB 9;	Length 339;
Best Local Similarity		99.6%;	Pred. No. 2.8e-90;		
Matches 259;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	VYLSECKTGKNGYRTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60		
Db	1	VYLSECKTGKNGYRTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60		
QY	61	DQGPWCYTTDPEKRYDYCDILLECEECMHCSGENYDGIKSKTMSGLECQAWDSQSPH	120		
Db	61	DQGPWCYTTDPEKRYDYCDILLECEECMHCSGENYDGIKSKTMSGLECQAWDSQSPH	120		
QY	121	GYIPSPFNKLNKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK	180		
Db	121	GYIPSPFNKLNKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK	180		
QY	181	GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	240		
Db	181	GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	240		
QY	241	TNSQVWEYCKIPSCDSSPV	260		
Db	241	TNSQVWEYCKIPSCDSSPV	260		

Search completed: August 29, 2006, 13:56:10  
Job time : 201 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2006, 14:14:04 ; Search time 33 Seconds  
(without alignments)  
539.087 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSEKCTGNGNYRGTMSK.....TNSQVRWEYKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	99.8	869	US-10-503-836-35	Sequence 35, Appl
2	1537	99.8	869	US-10-503-836-37	Sequence 37, Appl
3	1535	99.7	791	US-11-318-939-6	Sequence 6, Appli
4	1519.5	98.7	790	US-11-350-703-1	Sequence 1, Appli
5	1442	93.6	810	US-11-318-939-11	Sequence 11, Appl
6	1292	83.9	790	US-11-318-939-13	Sequence 13, Appl
7	1251	83.8	812	US-11-318-939-7	Sequence 7, Appli
8	1274	82.7	812	US-11-318-939-12	Sequence 12, Appl
9	1237	80.3	809	US-11-318-939-9	Sequence 9, Appli
10	794	51.6	475	US-11-328-070-14	Sequence 14, Appl
11	794	51.6	482	US-11-328-070-13	Sequence 13, Appl
12	794	51.6	486	US-11-328-070-2	Sequence 2, Appli
13	309.5	20.1	562	US-10-505-928-547	Sequence 547, App
14	309.5	20.1	562	US-11-183-218-26	Sequence 26, Appl
15	279.5	18.1	333	US-11-318-939-8	Sequence 8, Appli
16	278.5	18.1	703	US-10-503-836-39	Sequence 39, Appl
17	278.5	18.1	703	US-10-503-836-41	Sequence 41, Appl
18	263	17.1	338	US-11-318-939-10	Sequence 10, Appl
19	188.5	12.2	655	US-11-242-617-1	Sequence 1, Appli
20	170.5	11.1	653	US-11-242-617-2	Sequence 2, Appli
21	164	10.6	476	US-11-264-088-1	Sequence 1, Appli
22	164	10.6	476	US-11-311-475-1	Sequence 1, Appli
23	156	10.1	264	US-11-191-457-2	Sequence 2, Appli
24	150	9.7	27	US-11-134-871-698	Sequence 698, App
25	142	9.2	263	US-11-191-457-4	Sequence 4, Appli

26	135	8.8	431	6	US-10-505-928-465	Sequence 465, App
27	135	8.8	431	7	US-11-183-218-34	Sequence 34, Appl
28	135	8.8	477	7	US-11-264-088-2	Sequence 2, Appli
29	135	8.8	477	7	US-11-311-475-2	Sequence 12, Appl
30	134	8.7	138	7	US-11-330-353-12	Sequence 24, Appl
31	108	7.0	663	7	US-11-290-896-24	Sequence 2, Appli
32	106	6.9	685	7	US-11-175-714-2	Sequence 28, Appl
33	106	6.9	685	7	US-11-175-714-28	Sequence 34, Appl
34	106	6.9	685	7	US-11-175-714-32	Sequence 38, Appl
35	106	6.9	685	7	US-11-175-714-34	Sequence 36, Appl
36	106	6.9	685	7	US-11-175-714-36	Sequence 20, Appl
37	106	6.9	685	7	US-11-175-714-38	Sequence 2, Appli
38	106	6.9	685	7	US-11-178-724-20	Sequence 19, Appl
39	106	6.9	685	7	US-11-264-243-2	Sequence 40, Appl
40	106	6.9	685	7	US-11-071-796A-19	Sequence 25, Appl
41	105.5	6.9	429	7	US-11-290-896-40	Sequence 6, Appli
42	105.5	6.9	631	7	US-11-290-896-25	Sequence 22, Appl
43	104.5	6.8	2556	7	US-11-264-243-6	Sequence 16, Appl
44	102.5	6.7	2556	7	US-11-071-796A-22	
45	98.5	6.4	1953	7	US-11-264-243-16	

#### ALIGNMENTS

##### RESULT 1

US-10-503-836-35  
; Sequence 35, Application US/10503836  
; Publication No. US20060122374A1

GENERAL INFORMATION:  
; APPLICANT: Mertins, Peter

; APPLICANT: Celik, Ilhan

; APPLICANT: Kisker, Oliver

; APPLICANT: Sleep, Darrell

; APPLICANT: Hay, Joanna

; APPLICANT: Hauser, Hans-Peter

; TITLE OF INVENTION: ALBUMIN FUSED ANTI-ANGIOGENESIS PEPTIDES

; FILE REFERENCE: P27,972 USA

; CURRENT APPLICATION NUMBER: US/10/503,836

; CURRENT FILING DATE: 2004-08-06

; PRIOR APPLICATION NUMBER: PCT/IB03/00433

; PRIOR FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: 60/355,547

; PRIOR FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 35

; LENGTH: 869

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of the N-terminal angiotensin (non glycosylated) - albumin fusion protein

US-10-503-836-35

Query Match 99.8%; Score 1537; DB 6; Length 869;

Best Local Similarity 99.6%; Pred. No. 2.3e-120;

Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	VYLSEKCTGNGNYRGTMSKNGITCQKWSSTSPHRPFPSPATHPSEGLEENYCRNPDN	60
DB	25	VYLSEKCTGNGNYRGTMSKNGITCQKWSSTSPHRPFPSPATHPSEGLEENYCRNPDN	84
QY	61	DPQGPWCYTTDEPKRYDYCDILLECEECMHCSGENYDGKISKTMGLGECQAWDSQSPH	120
DB	85	DPQGPWCYTTDEPKRYDYCDILLECEECMHCSGENYDGKISKTMGLGECQAWDSQSPH	144
QY	121	GYIPSPFPNNLKNKNCRNPDRELRCWCTTDPNKKWELCDIPRCTPPSPSSGFTYQCLK	180
DB	145	GYIPSPFPNNLKNKNCRNPDRELRCWCTTDPNKKWELCDIPRCTPPSPSSGFTYQCLK	204
QY	181	GTGENTRGVAVTVSGHTCOHSAQTPHTRPENFPCKNLDENYCRNPDGKRAPWCHT	240



Db 205 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCKNLNDENYCRNPDGKRAPWCHT 264

QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 265 TNSQVRWEYCKIPSCDSSPV 284

RESULT 2

US-10-503-836-37

Sequence 37, Application US/10503836

Publication No. US20060122374A1

GENERAL INFORMATION:

APPLICANT: Mertins, Peter

APPLICANT: Celik, Ilhan

APPLICANT: Kisker, Oliver

APPLICANT: Sleep, Darrell

APPLICANT: Hay, Joanna

APPLICANT: Hauser, Hans-Peter

TITLE OF INVENTION: ALBUMIN FUSED ANTI-ANGIOGENESIS PEPTIDES

FILE REFERENCE: R27,972 USA

CURRENT APPLICATION NUMBER: US/10/503,836

CURRENT FILING DATE: 2004-08-06

PRIOR APPLICATION NUMBER: PCT/IB03/00433

PRIOR FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: 60/355,547

PRIOR FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 37

LENGTH: 869

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence at the C-terminal of albumin angiotensin (non glycosylated) - fusion protein

US-10-503-836-37

Query Match 99.8%; Score 1537; DB 6; Length 869;

Best Local Similarity 99.6%; Pred. No. 2.3e-120;

Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPDN 60

Db 610 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPDN 669

QY 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120

Db 670 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 729

QY 121 GYIPSKFPNKLKNGYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

Db 730 GYIPSKFPNKLKNGYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 789

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCKNLNDENYCRNPDGKRAPWCHT 240

Db 790 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCKNLNDENYCRNPDGKRAPWCHT 849

QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 850 TNSQVRWEYCKIPSCDSSPV 869

RESULT 3

US-11-318-939-6

Sequence 6, Application US/11318939

Publication No. US20060099671A1

GENERAL INFORMATION:

APPLICANT: Soff, Gerald

APPLICANT: Gately, Stephen T.

APPLICANT: Twardowski, Przemyslaw

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN

FILE REFERENCE: 4228-1-1-1

CURRENT APPLICATION NUMBER: US/11/318,939

QY 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPDN 60

Db 79 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPDN 138

QY 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120

Db 139 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 198

QY 121 GYIPSKFPNKLKNGYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

Db 199 GYIPSKFPNKLKNGYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 258

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCKNLNDENYCRNPDGKRAPWCHT 240

Db 259 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCKNLNDENYCRNPDGKRAPWCHT 318

QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 319 TNSQVRWEYCKIPSCDSSPV 338

RESULT 4

US-11-350-703-1

Sequence 1, Application US/11350703

Publication No. US20060135428A1

GENERAL INFORMATION:

APPLICANT: Bridon, Dominique P.

APPLICANT: Rasamoeliso, Michele

APPLICANT: Thibaudeau, Karen

APPLICANT: Huang, Xicai

APPLICANT: Bellevue, Richard

TITLE OF INVENTION: LONG LASTING ANTI-ANGIOGENIC PEPTIDES

FILE REFERENCE: 500862001401

CURRENT APPLICATION NUMBER: US/11/350,703

CURRENT FILING DATE: 2006-02-08

PRIOR APPLICATION NUMBER: US 09/623,543

PRIOR FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: PCT/IB00/00763

PRIOR FILING DATE: 2000-05-17

PRIOR APPLICATION NUMBER: 60/134,406

PRIOR FILING DATE: 1999-05-17

PRIOR APPLICATION NUMBER: 09/657,431

PRIOR FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: 60/153,406

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: 60/159,783

PRIOR FILING DATE: 1999-10-15

NUMBER OF SEQ ID NOS: 67

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 790

TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-350-703-1

Query Match 98.7%; Score 1519.5; DB 7; Length 790;  
Best Local Similarity 99.2%; Pred. No. 6e-119;  
Matches 258; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60  
DB 79 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 137  
QY 61 DQGPWCYTTDPEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDSQSPHAAH 120  
DB 138 DQGPWCYTTDPEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDSQSPHAAH 197  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
DB 198 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 257  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 258 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 317  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 318 TNSQVRWEYCKIPSCDSSPV 337

## RESULT 5

US-11-318-939-11  
; Sequence 11, Application US/11318939  
; Publication No. US20060099671A1  
; GENERAL INFORMATION:  
; APPLICANT: Soff, Gerald  
; APPLICANT: Gately, Stephen T.  
; APPLICANT: Twardowski, Przemyslaw

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN  
; FILE REFERENCE: 4228-1-1-1  
; CURRENT APPLICATION NUMBER: US/11/318,939  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/09/500,397  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; TYPE: PRT  
; ORGANISM: Macaca mulatta

## US-11-318-939-11

Query Match 93.6%; Score 1442; DB 7; Length 810;  
Best Local Similarity 93.1%; Pred. No. 1.8e-112;  
Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60  
DB 98 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157  
QY 61 DQGPWCYTTDPEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDSQSPHAAH 120  
DB 158 DQGPWCYTTDPEERFDYCDIPECEBECMHCSENGYDGIKSKTMSGLECOAMDSQSPHAAH 217  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
DB 218 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 277

QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 278 GTGENYRGNAVTVSGHTCHGWSAQTPTHTNRTPENFPCKNLNDENYCRNPDGKRAPWCHT 337  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 338 TNSQVRWEYCKIPSCDSSPV 357

## RESULT 6

US-11-318-939-13  
; Sequence 13, Application US/11318939  
; Publication No. US20060099671A1  
; GENERAL INFORMATION:  
; APPLICANT: Soff, Gerald  
; APPLICANT: Gately, Stephen T.  
; APPLICANT: Twardowski, Przemyslaw  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN  
; FILE REFERENCE: 4228-1-1-1  
; CURRENT APPLICATION NUMBER: US/11/318,939  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/09/500,397  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 790  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-11-318-939-13

Query Match 83.9%; Score 1292; DB 7; Length 790;  
Best Local Similarity 81.4%; Pred. No. 5.6e-100;  
Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60  
DB 79 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 138  
QY 61 DQGPWCYTTDPEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDSQSPHAAH 120  
DB 139 DEKGPWCYTTDPEKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAMDSQSPHAAH 198  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
DB 199 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 258  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 259 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 318  
QY 241 TNSQVRWEYCKIPSCDSSPV 258  
DB 319 TNSQVRWEYCKIPSCDSSPV 336

## RESULT 7

US-11-318-939-7  
; Sequence 7, Application US/11318939  
; Publication No. US20060099671A1  
; GENERAL INFORMATION:  
; APPLICANT: Soff, Gerald  
; APPLICANT: Gately, Stephen T.  
; APPLICANT: Twardowski, Przemyslaw  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN  
; FILE REFERENCE: 4228-1-1-1

```
; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Bos taurus
; US-11-318-939-7

Query Match      83.8%; Score 1291; DB 7; Length 812;
Best Local Similarity 80.8%; Pred. No. 6.9e-100;
Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCKQWSSTSPHRPFPSPATHPSEGLEENYCRNPDN 60
Db 105 IYLLSECKTGNGQTYRGTTAETKSGVTCQKWSATSHVPKPSPEKFPPLAGLEENYCRNPDN 164
QY 61 DQGPWCYTTDPKRYDYCDILECEECMHCSGENYDGIKSKTMSGLECOAWDSQSPHAH 120
Db 165 DENGWCYTTDPKRYDYCDIPECEDKMHCSGENYEGKIAKTMGRDCQAWDSQSPHAH 224
QY 121 GYIPSKFPNNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
Db 225 GYIPSKFPNNLKNYCRNPDGEPRWCFTTDPQKRWECFCDIPRCTTTPPSSGPTYQCLK 284
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
Db 285 GTGKNYGVTVAVTSGHTCQWSEQTQPHKHNTPENFPCKNLNDENYCRNPDGKAPWCYT 344
QY 241 TNSQVRWEYCKIPSCDSSV 260
Db 345 TNSQVRWEYCTIPSCESSPL 364

RESULT 8
US-11-318-939-12
; Sequence 12, Application US/11318939
; Publication No. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Gately, Stephen T.
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
; FILE REFERENCE: 4228-1-1-1
; CURRENT APPLICATION NUMBER: US/11/318,939
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Erinaceus europaeus
; US-11-318-939-9

Query Match      80.3%; Score 1237; DB 7; Length 809;
Best Local Similarity 77.9%; Pred. No. 2.2e-95;
Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCKQWSSTSPHRPFPSPATHPSEGLEENYCRNPDN 60
Db 98 MYLSECKGVNGKYRGTYGTSKTKGTCQKWSATPHKPRFSPDENPSEGLDQNYCRNPDN 157
QY 61 DQGPWCYTTDPKRYDYCDILECEECMHCSGENYDGIKSKTMSGLECOAWDSQSPHAH 120
Db 158 DPKGWCYTMDEPVEYECIQQCEDECMHCSGQNYVGKISRTMSGLECOQPDWSQIPH 217
QY 121 GYIPSKFPNNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
Db 218 GFIPSKFPNNLKNYCRNPDGEPRWCFTTDMNRKWEYCDIPRCTTTPPSSGPTYQCLK 277
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
Db 278 GNGEYQGNVAVTVSGLTCQWSEQSPHHRHDPENFPCKNLNDENYCRNPDGEPAPWCT 337
QY 241 TNSQVRWEYCKIPSCDSS 258
Db 338 TDSQLRWEYCEIPSCSS 355

RESULT 9
US-11-318-939-9
; Sequence 9, Application US/11318939
; Publication No. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Gately, Stephen T.
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
; FILE REFERENCE: 4228-1-1-1
; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Erinaceus europaeus
; US-11-318-939-9

Query Match      80.3%; Score 1237; DB 7; Length 809;
Best Local Similarity 77.9%; Pred. No. 2.2e-95;
Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCKQWSSTSPHRPFPSPATHPSEGLEENYCRNPDN 60
Db 98 MYLSECKGVNGKYRGTYGTSKTKGTCQKWSATPHKPRFSPDENPSEGLDQNYCRNPDN 157
QY 61 DQGPWCYTTDPKRYDYCDILECEECMHCSGENYDGIKSKTMSGLECOAWDSQSPHAH 120
Db 158 DPKGWCYTMDEPVEYECIQQCEDECMHCSGQNYVGKISRTMSGLECOQPDWSQIPH 217
QY 121 GYIPSKFPNNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
Db 218 GFIPSKFPNNLKNYCRNPDGEPRWCFTTDMNRKWEYCDIPRCTTTPPSSGPTYQCLK 277
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
Db 278 GNGEYQGNVAVTVSGLTCQWSEQSPHHRHDPENFPCKNLNDENYCRNPDGEPAPWCT 337
QY 241 TNSQVRWEYCKIPSCDSS 258
Db 338 TDSQLRWEYCEIPSCSS 355
```



; Sequence 547, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 547  
; LENGTH: 562  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-547

Query Match 20.1%; Score 309.5; DB 6; Length 562;  
Best Local Similarity 34.1%; Pred. No. 3.2e-18;  
Matches 77; Conservative 23; Mismatches 103; Indels 23; Gaps 9;  
QY 46 PSEGLEENYCRNPNDPQGPWCYTTD-----PEKRYDYCDILECEBECMHCSGENYDGI 100  
DB 82 PVKSCSEPRCFNGGTCCQA--LYFSDFVCQCPGAGKCEIDTRATCYEDQGISYRGTW 139  
QY 101 SKTMSGLECOANDS-----QSPHAGYIPSKFNNKLNKNNYCRNPDELSPWCFTTDPNK- 155  
DB 140 STAESGAECTNWNSSALAKPYS--GRRPDAILRLGLGNHNYCRNPDSDKPCYVFKAGY 198  
QY 156 RWELCDIPRCTTTPPPSSGPTYOCLKGTGENYRGNVAVTVSGHTCQHSQAOTPHHTERTPE 215  
DB 199 SSEFCSTPAC-----SEGNS--DCYFGNGSAYRGTHSLTESGASCLPWNMSMILIGKYTTAQ 252  
QY 216 NFPCKNL---DENYCRNPDGKRAPWCHT--TNSQVRWEYCKIPSCDS 257  
DB 253 NPSAQLGLGKHNYCRNPDGDAKWPCHVLKNRRLTWECYDVPSCST 298

## RESULT 14

US-11-183-218-26  
; Sequence 26, Application US/11183218  
; Publication No. US20060088906A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DeFrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bowe, Caryne  
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND  
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN  
; FILE REFERENCE: 040853-01-5083-US02  
; CURRENT APPLICATION NUMBER: US/11/183,218  
; CURRENT FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US 10/410,945  
; PRIOR FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: PCT/US02/32263  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/334,301

; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/334,233  
; PRIOR FILING DATE: 2001-11-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 562  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-183-218-26

Query Match 20.1%; Score 309.5; DB 7; Length 562;  
Best Local Similarity 34.1%; Pred. No. 3.2e-18;  
Matches 77; Conservative 23; Mismatches 103; Indels 23; Gaps 9;  
QY 46 PSEGLEENYCRNPNDPQGPWCYTTD-----PEKRYDYCDILECEBECMHCSGENYDGI 100  
DB 82 PVKSCSEPRCFNGGTCCQA--LYFSDFVCQCPGAGKCEIDTRATCYEDQGISYRGTW 139  
QY 101 SKTMSGLECOANDS-----QSPHAGYIPSKFNNKLNKNNYCRNPDELSPWCFTTDPNK- 155  
DB 140 STAESGAECTNWNSSALAKPYS--GRRPDAILRLGLGNHNYCRNPDSDKPCYVFKAGY 198  
QY 156 RWELCDIPRCTTTPPPSSGPTYOCLKGTGENYRGNVAVTVSGHTCQHSQAOTPHHTERTPE 215  
DB 199 SSEFCSTPAC-----SEGNS--DCYFGNGSAYRGTHSLTESGASCLPWNMSMILIGKYTTAQ 252  
QY 216 NFPCKNL---DENYCRNPDGKRAPWCHT--TNSQVRWEYCKIPSCDS 257  
DB 253 NPSAQLGLGKHNYCRNPDGDAKWPCHVLKNRRLTWECYDVPSCST 298

## RESULT 15

US-11-318-939-8  
; Sequence 8, Application US/11318939  
; Publication No. US20060099671A1  
; GENERAL INFORMATION:  
; APPLICANT: Soff, Gerald  
; APPLICANT: Gately, Stephen T.  
; APPLICANT: Twardowski, Przemyslaw  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN  
; FILE REFERENCE: 4228-1-1-1  
; CURRENT APPLICATION NUMBER: US/11/318,939  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/09/500,397  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-09-17  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 08/991,761  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-09-17  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-11-318-939-8

Query Match 18.1%; Score 279.5; DB 7; Length 333;  
Best Local Similarity 48.5%; Pred. No. 5.8e-16;  
Matches 47; Conservative 13; Mismatches 36; Indels 1; Gaps 1;  
QY 4 SECKTGNGKNYRGTGMSKTKNGITCKWSTSPHRRP--FSPATHPSGLBENYCRNPNDP 62  
DB 2 SDCMFNGKGYRGKATTTVMGIPCOEWAAQEPHRSIFTPETNPQAGLEKNYCRNPDGV 61  
QY 63 QGFWCYTTDPEKRYDYCDILECEBECMHCSGENYDGI 99  
DB 62 NGFWCYTWNQRKLDYCDVPCVSTSFDCGKQVPEPK 98

Search completed: August 29, 2006, 14:17:35  
Job time : 34 secs

**This Page Blank (uspto)**



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 29, 2006, 14:13:24 ; Search time 181 Seconds  
(without alignments)  
665.392 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKNGRTWSK.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	4	US-10-131-241-61
2	1535	99.7	303	5	US-10-810-262-11
3	1535	99.7	339	3	US-09-788-142-3
4	1535	99.7	339	3	US-09-761-120-3
5	1535	99.7	339	3	US-09-335-325-3
6	1535	99.7	339	4	US-10-131-241-3
7	1535	99.7	339	4	US-10-127-066-3
8	1535	99.7	339	4	US-10-402-364-3
9	1535	99.7	339	4	US-10-401-108-3
10	1535	99.7	339	6	US-11-010-874-3
11	1535	99.7	363	4	US-10-292-418-11
12	1535	99.7	378	3	US-09-873-676-1
13	1535	99.7	378	3	US-09-335-325-42
14	1535	99.7	378	4	US-10-131-241-42
15	1535	99.7	378	4	US-10-127-066-42
16	1535	99.7	391	4	US-10-304-287-7
17	1535	99.7	391	4	US-10-415-012-1
18	1535	99.7	391	4	US-10-735-577-7
19	1535	99.7	394	4	US-10-304-287-8
20	1535	99.7	394	4	US-10-415-012-2
21	1535	99.7	394	4	US-10-735-577-8
22	1535	99.7	484	4	US-10-135-872B-7
23	1535	99.7	567	4	US-10-741-601-413
24	1535	99.7	567	5	US-10-995-561-764
25	1535	99.7	569	3	US-09-946-893-5
26	1535	99.7	571	3	US-09-946-893-8
27	1535	99.7	576	3	US-09-946-893-6

28	1535	99.7	579	4	US-10-449-609-7	Sequence 7, Appli
29	1535	99.7	714	4	US-10-415-012-8	Sequence 8, Appli
30	1535	99.7	714	5	US-10-503-910-18	Sequence 18, Appli
31	1535	99.7	791	3	US-09-967-386-1	Sequence 1, Appli
32	1535	99.7	791	4	US-10-304-287-1	Sequence 1, Appli
33	1535	99.7	791	4	US-10-360-101-257	Sequence 257, App
34	1535	99.7	791	4	US-10-778-423-1	Sequence 1, Appli
35	1535	99.7	791	4	US-10-753-646-1	Sequence 1, Appli
36	1535	99.7	791	4	US-10-735-577-1	Sequence 1, Appli
37	1535	99.7	791	5	US-10-729-475-10	Sequence 10, Appli
38	1535	99.7	791	5	US-10-503-910-17	Sequence 17, Appli
39	1535	99.7	791	6	US-11-056-621-4	Sequence 4, Appli
40	1535	99.7	798	6	US-11-108-459-8	Sequence 8, Appli
41	1535	99.7	799	5	US-10-503-910-8	Sequence 8, Appli
42	1535	99.7	803	5	US-10-503-910-10	Sequence 10, Appli
43	1535	99.7	810	3	US-09-946-893-2	Sequence 2, Appli
44	1535	99.7	810	4	US-10-193-656-2	Sequence 2, Appli
45	1535	99.7	810	4	US-10-237-144-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-131-241-61

; Sequence 61, Application US/10131241

; Publication No. US20030012792A1

; GENERAL INFORMATION:

; APPLICANT: Holaday, John W.

; APPLICANT: Fortier, Anne H.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

; FILE REFERENCE: 05213-0344 43170-271565

; CURRENT APPLICATION NUMBER: US/10/131,241

; PRIOR FILING DATE: 2002-07-22

; PRIOR APPLICATION NUMBER: US 09/413,049

; PRIOR FILING DATE: 1999-10-06

; PRIOR APPLICATION NUMBER: US 09/316,802

; PRIOR FILING DATE: 1999-05-21

; PRIOR APPLICATION NUMBER: US 60/086,586

; PRIOR FILING DATE: 1998-05-22

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 61

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-131-241-61

Query Match 100.0%; Score 1540; DB 4; Length 260;

Best Local Similarity 100.0%; Pred. No. 2.3e-120;

Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VYLSECKTGNGKNGRTWSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
DB	1	VYLSECKTGNGKNGRTWSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
QY	61	DQGGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLECQAWDSQSPHAH	120
DB	61	DQGGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLECQAWDSQSPHAH	120
QY	121	GYIPSKFPNKLKNGYCRNPDRRLPWCCTTDPNKRWELCDIPRCTTTPPSSGPTVQCLK	180
DB	121	GYIPSKFPNKLKNGYCRNPDRRLPWCCTTDPNKRWELCDIPRCTTTPPSSGPTVQCLK	180
QY	181	GTGNGYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGGRAPWCHT	240
DB	181	GTGNGYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGGRAPWCHT	240
QY	241	TNSQVRWEYCKIPSCDSSPV 260	
DB	241	TNSQVRWEYCKIPSCDSSPV 260	

RESULT 2  
US-10-810-262-11  
; Sequence 11, Application US/10810262  
; Publication No. US20040234505A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSMAN, SUSAN MARY  
; APPLICANT: BINLEY, KATIE  
; TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF  
; FILE REFERENCE: 674523-2029.1  
; CURRENT APPLICATION NUMBER: US/10/810,262  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: 09/787,562  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB99/03181  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/GB98/02885  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: GB 9901906.9  
; PRIOR FILING DATE: 1999-01-28  
; PRIOR APPLICATION NUMBER: GB 9903538.8  
; PRIOR FILING DATE: 1999-02-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 11  
; LENGTH: 303  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-810-262-11

Query Match 99.7%; Score 1535; DB 5; Length 303;  
Best Local Similarity 99.6%; Pred. No. 7.2e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
Db 33 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 92  
  
QY 61 DQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 120  
Db 93 DQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 152  
  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 153 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 212  
  
QY 181 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240  
Db 213 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHTNPFCNLDENYCRNPDGKRAPWCHT 272  
  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 273 TNSQVRWEYCKIPSCDSSPV 292

RESULT 3  
US-09-788-142-3  
; Sequence 3, Application US/09788142  
; Patent No. US20010029246A1  
; GENERAL INFORMATION:  
; APPLICANT: Folkman, M. Judah  
; O'Reilly, Michael  
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1769  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/788,142  
FILING DATE: 16-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/866,735  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05940-0129  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 818-3700  
TELEFAX: (404) 818-3799  
INFORMATION FOR SEQ ID NO: 3:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-788-142-3

Query Match 99.7%; Score 1535; DB 3; Length 339;  
Best Local Similarity 99.6%; Pred. No. 8.2e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
  
QY 61 DQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 120  
Db 61 DQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGIKSKTMSGLECQAWDSQSPHAH 120  
  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
  
QY 181 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHTNPFCNLDENYCRNPDGKRAPWCHT 240  
  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 4  
US-09-761-120-3  
; Sequence 3, Application US/09761120  
; Patent No. US20020037847A1  
; GENERAL INFORMATION:  
; APPLICANT: Folkman, M. Judah  
; O'Reilly, Michael  
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen  
; FILE REFERENCE: 05940-0151 (43171-252068)  
; CURRENT APPLICATION NUMBER: US/09/761,120  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/309,821  
; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 08/866,735  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 3  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-120-3

Query Match 99.7%; Score 1535; DB 3; Length 339;  
Best Local Similarity 99.6%; Pred. No. 8.2e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSGENYDGKISKTMGLECOAWDSQSPHAAH 120  
DB 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSGENYDGKISKTMGLECOAWDSQSPHAAH 120  
QY 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180  
DB 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180  
QY 181 GTGENYRGNAVTVSGHTCQHWSAOTPHTHRTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCQHWSAOTPHTHRTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

## RESULT 5

US-09-335-325-3  
; Sequence 3, Application US/09335325  
; Patent No. US20020164717A1  
; GENERAL INFORMATION:  
; APPLICANT: Folkman, M. Judah  
; O'Reilly, Micheal  
; Cao, Yihai  
; Sim, B. Kim Lee  
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.  
; ZIP: 30303-1769  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/335,325  
; FILING DATE: 17-Jun-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,788  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren, William L.  
; REGISTRATION NUMBER: 36,714  
; REFERENCE/DOCKET NUMBER: 05213-0126  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: Angiostatin fragment  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 3; Length 339;  
Best Local Similarity 99.6%; Pred. No. 8.2e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSGENYDGKISKTMGLECOAWDSQSPHAAH 120  
DB 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSGENYDGKISKTMGLECOAWDSQSPHAAH 120  
QY 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180  
DB 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180  
QY 181 GTGENYRGNAVTVSGHTCQHWSAOTPHTHRTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCQHWSAOTPHTHRTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

## RESULT 6

US-10-131-241-3  
; Sequence 3, Application US/10131241  
; Publication No. US20030012792A1  
; GENERAL INFORMATION:  
; APPLICANT: Holaday, John W.  
; APPLICANT: Fortier, Anne H.  
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers  
; FILE REFERENCE: 05213-0344 43170-271565  
; CURRENT APPLICATION NUMBER: US/10/131,241  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US 09/413,049  
; PRIOR FILING DATE: 1999-10-06  
; PRIOR APPLICATION NUMBER: US 09/316,802  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: US 60/086,586  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-131-241-3  
Query Match 99.7%; Score 1535; DB 4; Length 339;  
Best Local Similarity 99.6%; Pred. No. 8.2e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60

Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPAH 120  
Db 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPAH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GYIPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

## RESULT 7

US-10-127-066-3

; Sequence 3, Application US/10127066  
; Publication No. US20030064926A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Reilly, Michael S.  
; APPLICANT: Folkman, M. Judah  
; APPLICANT: Cao, Yihai  
; APPLICANT: Sim, Kim Lee  
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
; FILE REFERENCE: 05213-0612 43170-272529  
; CURRENT APPLICATION NUMBER: US/10/127,066  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-127-066-3

Query Match 99.7%; Score 1535; DB 4; Length 339;  
Best Local Similarity 99.6%; Pred. No. 8.2e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPAH 120  
Db 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPAH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GYIPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

## RESULT 8

US-10-402-364-3

; Sequence 3, Application US/10402364  
; Publication No. US20040002459A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Reilly, Michael  
; APPLICANT: Folkman, M. Judah  
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen

; FILE REFERENCE: 05213-2151 (43170-252068)  
; CURRENT APPLICATION NUMBER: US/10/402,364  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: US/09/761,120A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/309,821  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 08/866,735  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-402-364-3

Query Match 99.7%; Score 1535; DB 4; Length 339;  
Best Local Similarity 99.6%; Pred. No. 8.2e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60  
QY 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPAH 120  
Db 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPAH 120  
QY 121 GYIPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
Db 121 GYIPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 241 TNSQVRWEYCKIPSCDSSPV 260

## RESULT 9

US-10-401-108-3

; Sequence 3, Application US/10401108  
; Publication No. US20040023877A1  
; GENERAL INFORMATION:  
; APPLICANT: Folkman, M. Judah  
; O'Reilly, Michael  
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1769  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/401,108  
; FILING DATE: 27-Mar-2003  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/866,735  
; FILING DATE: 30-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren, William L.  
; REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05940-0129  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 818-3700  
 TELEFAX: (404) 818-3799  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 339 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 IMMEDIATE SOURCE:  
 CLONE: Angiostatin fragment  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 99.7%; Score 1535; DB 4; Length 339;  
 Best Local Similarity 99.6%; Pred. No. 8.2e-120;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 VYLSEKGTGKNGYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSEKGTGKNGYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGSLGCQAWDSQSPH 120
DB 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGSLGCQAWDSQSPH 120
QY 121 GYIPSPFPNNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
DB 121 GYIPSPFPNNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

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## RESULT 10

US-11-010-874-3

Sequence 3, Application US/11010874  
 Publication No. US20050250694A1

## GENERAL INFORMATION:

APPLICANT: Ma, Jian-King  
 TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND  
 TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME  
 FILE REFERENCE: 5820.656  
 CURRENT APPLICATION NUMBER: US/11/010,874  
 PRIOR FILING DATE: 2004-12-13  
 PRIOR FILING DATE: 2004-12-13  
 PRIOR FILING DATE: 2004-10-12  
 PRIOR FILING DATE: 2004-10-12  
 PRIOR FILING DATE: 2003-10-10  
 PRIOR FILING DATE: 2003-10-10  
 PRIOR FILING DATE: 2003-12-11  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 3

LENGTH: 339

TYPE: PRT

ORGANISM: Homo sapiens

US-11-010-874-3

Query Match 99.7%; Score 1535; DB 6; Length 339;  
 Best Local Similarity 99.6%; Pred. No. 8.2e-120;

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Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSEKGTGKNGYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSEKGTGKNGYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGSLGCQAWDSQSPH 120
DB 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGSLGCQAWDSQSPH 120
QY 121 GYIPSPFPNNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
DB 121 GYIPSPFPNNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

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## RESULT 11

US-10-292-418-11

Sequence 11, Application US/10292418  
 Publication No. US20030139365A1

## GENERAL INFORMATION:

APPLICANT: Lo, Kin-Ming  
 APPLICANT: Li, Yue  
 APPLICANT: Gillies, Stephen D  
 TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as  
 TITLE OF INVENTION: Immunofusins  
 FILE REFERENCE: LEX-006C1  
 CURRENT APPLICATION NUMBER: US/10/292,418  
 CURRENT FILING DATE: 2002-11-12  
 PRIOR APPLICATION NUMBER: 09/383,315  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: US 60/097,883  
 PRIOR FILING DATE: 1998-08-25  
 NUMBER OF SEQ ID NOS: 54  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 11

LENGTH: 363

TYPE: PRT

ORGANISM: Homo sapiens

US-10-292-418-11

Query Match 99.7%; Score 1535; DB 4; Length 363;

Best Local Similarity 99.6%; Pred. No. 8.9e-120;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 VYLSEKGTGKNGYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 2 VYLSEKGTGKNGYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 61
QY 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGSLGCQAWDSQSPH 120
DB 62 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGSLGCQAWDSQSPH 121
QY 121 GYIPSPFPNNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
DB 122 GYIPSPFPNNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 181
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
DB 182 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 241
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 242 TNSQVRWEYCKIPSCDSSPV 261

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RESULT 12

US-09-873-676-1  
; Sequence 1, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: Macdonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 378  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-873-676-1

Query Match 99.7%; Score 1535; DB 3; Length 378;  
Best Local Similarity 99.6%; Pred. No. 9.3e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
Db 6 VYLSECKTGNKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 65  
QY 61 DQGPWCYTTDPEKRYDYCDILECEECCHSCGENYDGIKSKTMSGLECQAWDSQSPHAH 120  
Db 66 DQGPWCYTTDPEKRYDYCDILECEECCHSCGENYDGIKSKTMSGLECQAWDSQSPHAH 125  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180  
Db 126 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 185  
QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPTHTNTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
Db 186 GTGENYRGNAVTVSGHTCQHWSAQTPTHTNTPENFPCKNLDENYCRNPDGKRAPWCHT 245  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 13

US-09-335-325-42  
; Sequence 42, Application US/09335325  
; Patent No. US20020164717A1  
; GENERAL INFORMATION:  
; APPLICANT: Folkman, M. Judah  
; Cao, Yihai  
; Sim, B. Kim Lee  
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.  
; ZIP: 30303-1769  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/335,325

FILING DATE: 17-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: K1-4BKLS  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-335-325-42

Query Match 99.7%; Score 1535; DB 3; Length 378;  
Best Local Similarity 99.6%; Pred. No. 9.3e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60  
Db 6 VYLSECKTGNKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 65  
QY 61 DQGPWCYTTDPEKRYDYCDILECEECCHSCGENYDGIKSKTMSGLECQAWDSQSPHAH 120  
Db 66 DQGPWCYTTDPEKRYDYCDILECEECCHSCGENYDGIKSKTMSGLECQAWDSQSPHAH 125  
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180  
Db 126 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 185  
QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPTHTNTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
Db 186 GTGENYRGNAVTVSGHTCQHWSAQTPTHTNTPENFPCKNLDENYCRNPDGKRAPWCHT 245  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 14

US-10-131-241-42  
; Sequence 42, Application US/10131241  
; Publication No. US20030012792A1  
; GENERAL INFORMATION:  
; APPLICANT: Holaday, John W.  
; APPLICANT: Fortier, Anne H.  
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
; FILE REFERENCE: 05213-0344 43170-271565  
; CURRENT APPLICATION NUMBER: US/10/131,241  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US 09/413,049  
; PRIOR FILING DATE: 1999-10-06  
; PRIOR APPLICATION NUMBER: US 09/316,802  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: US 60/086,586  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 65

Search completed: August 29, 2006, 14:16:57  
Job time : 182 secs

Query Match	99.7%	Score 1535;	DB 4;	Length 378;
Best Local Similarity	99.6%	Pred. No. 9.3e-120;		
Matches 259; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	VYLSECKTGNKNGYGTMTSKTNGITCQKWSSTSPHPRPSPATHPSGLEGLEENYCRNP	60
Db	6	VYLSECKTGNKNGYGTMTSKTNGITCQKWSSTSPHPRPSPATHPSGLEGLEENYCRNP	65
Qy	61	DPOGPWCYTTPDPEKRYDYCDILECEECECMHCSGENYDGKISKTMGSLGLECQAWDSQSPH	120
Db	66	DPOGPWCYTTPDPEKRYDYCDILECEECECMHCSGENYDGKISKTMGSLGLECQAWDSQSPH	125
Qy	121	GYTPSKFPNNLKNYCRNPDRRLRPMCFTTDPNKRWELCDIPRCTTTPSPSSGGTYOCLK	180
Db	126	GYTPSKFPNNLKNYCRNPDRRLRPMCFTTDPNKRWELCDIPRCTTTPSPSSGGTYOCLK	185
Qy	181	GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENPCKNLNDENYCRNPDGKRAPWCHT	240
Db	186	GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENPCKNLNDENYCRNPDGKRAPWCHT	245
Qy	241	TNSQVRWEYCKIPSCDSSPV	260
Db	246	TNSQVRWEYCKIPSCDSSPV	265

**RESULT 15**

```

US-10-127-066-42
; Sequence 42, Application US/10127066
; Publication No. US20030064926A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; APPLICANT: Folkman, M. Judah
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; FILE REFERENCE: 05213-0612 43170-272529
; CURRENT APPLICATION NUMBER: US/10/127,066
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-127-066-42

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Query Match	99.7%	Score 1535;	DB 4;	Length 378;
Best Local Similarity	99.6%	Pred. No. 9.3e-120;		
Matches 259; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	VYLSECTGNGKNGYGTWSTKTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRPNPDN	60
Db	6	VYLSECTGNGKNGYGTWSTKTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRPNPDN	65
Qy	61	DQGPWCYCTTDPKRYDYCDILCEEBCMHCSGNYDGKISKTMGSLCQAWDSQSPHAF	120
Db	66	DQGPWCYCTTDPKRYDYCDILCEEBCMHCSGNYDGKISKTMGSLCQAWDSQSPHAF	125
Qy	121	GYIPSKFPKNLKNKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPSSGGTYOCLK	180
Db	126	GYIPSKFPKNLKNKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPSSGGTYOCLK	185
Qy	181	GTGNGYGNVAVTVSGHTCOHWSAQTPHTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	240
Db	186	GTGNGYGNVAVTVSGHTCOHWSAQTPHTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	245



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